

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2005, 15:35:11 ; Search time 43.7895 Seconds
(without alignments)
1413.163 Million cell updates/sec

Title: US-09-904-954-4_COPY_1_160
Perfect score: 879
Sequence: 1 MRLPLRLRTVLMMAAFLGSPPL.....SGQCRLRLQVSVCKEKRSSES 160

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	100.0	201	2 AAR71482	Aar71482 Human hek

ALIGNMENTS

RESULT 1
AAR71482
ID AAR71482 standard; protein; 201 AA.
XX
AC AAR71482;
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-1995 (first entry)
XX
DE Human hek-L protein.
XX
KW Ligand; cell surface; tyrosine kinase receptor; tumorigenesis; immunogen.
XX
OS Homo sapiens.
XX
OS
XX
FH Key
FH Peptide
FT 1..22
FT /note="signal peptide"
FT 23..201
FT Protein

XX	WO9506065-A1.
PN	
XX	
PD	02-MAR-1995.
XX	
XX	17-AUG-1994; 94WO-US009282.
XX	
PR	20-AUG-1993; 93US-00109745.
PR	30-AUG-1993; 93US-00114426.
PR	03-DEC-1993; 93US-00161132.
PR	09-MAY-1994; 94US-00240124.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Beckmann MP, Cerretti DP;
XX	
XX	WPI; 1995-106811/14.
DR	N-PSDB; AAQ85888.
XX	
PT	New isolated DNA encoding hek-L protein or its fusion products - useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukaemia cells.
PS	Claim 21; Page 38; 45pp; English.
XX	
CC	The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the alk tyrosine kinase receptors. See also AAR71481. (Updated on 25-MAR-2003 to correct PN field.)
XX	
SO	Sequence 201 AA:
QY	Query Match 100.0%; Score 879; DB 2; Length 201;
Db	Best Local Similarity 100.0%; Pred. No. 3.4e-93;
QY	Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MRLPLRLRTVLMMAAFLGSPPLRGGSSLRHHVYVMNSNPRLLRGAIVELGINDYLDIYCPH 60
QY	1 YEGGPPPEGETFALVMDWPGYESSCAEGPRAYKRWVCSLIPFGHVQFSEKIQRFPTPSL 120
Db	61 YEGGPPPEGETFALVMDWPGYESSCAEGPRAYKRWVCSLIPFGHVQFSEKIQRFPTPSL 120
QY	121 GFEFLPGFTYYIISVPTPESSGQCRLRLQVSVCKEKRSSES 160
Db	121 GFEFLPGFTYYIISVPTPESSGQCRLRLQVSVCKEKRSSES 160

Search completed: April 19, 2005, 23:13:33
Job time : 43.7895 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 09:30:04 ; Search time 3056 Seconds
(without alignments)
8183.329 Million cell updates/sec

Title: US-09-904-954-1_COPY_140_796
Perfect score: 657
Sequence: 1 CTGCTGGCCCAAGGGCCCGG.....TCATGACGTTCTGGCCTCC 657

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing First 1500 summaries

Database :

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hnc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	657	100.0	1741	CR607482	CR607482 full-leng
2	645	98.2	871	BX419695	BX419695 BX419695
3	622.6	94.8	1100	AL533153	AL533153 AL533153
4	598.4	91.1	726	AL527972	AL527972 AL527972
5	587.2	89.4	1629	CR597504	CR597504 full-leng

ALIGNMENTS

RESULT 1
CR607482
LOCUS CR607482 1741 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODN03Y119 of Adult brain of Homo sapiens (human).
ACCESSION CR607482 GI:50488289
VERSION CR607482.1
KEYWORDS HTC; CNSLT; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1741)
AUTHORS Li, W. B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization
UNPUBLISHED
CONTACT: Peng Liang Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue
Foster City, CA 94024
2 (bases 1 to 1741)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1741
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN03Y119"
/issue_type="Adult brain"
/plasmid="pCMVSPORT_6"

COMMENT

FEATURES
source

ORIGIN

Query Match 100.0%; Score 657; DB 3; Length 1741;
Best Local Similarity 100.0%; Pred. No. 6.2e-143;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTGCTGGCCCAAGGGCCCGGCTGGGAAACCCGGATGGCGTGTCTGGAACAGC	60
Db	122	CTGCTGGCCCAAGGGCCCGGCTGGGAAACCCGGATGGCGTGTCTGGAACAGC	181
Qy	61	TCCAACCAAGCACTGCGCGGAGAGGGCTTACACCGGTGAACTGAAAGCATATCTG	120
Db	182	TCCAACCAAGCACTGCGCGGAGAGGGCTTACACCGGTGAAAGCATATCTG	241
Qy	121	GATATTTTACGTGCGCGCACTAACAGCTGGGGGTGGCCCGGGGGCGGACCGGGCC	180
Db	242	GATATTTTACGTGCGCGCACTAACAGCTGGGGGTGGCCCGGGGGCGGACCGGGCC	301
Qy	181	GGAGGGGGGCAAGGACGTAAGTGTGTGTATAGTGTGAGCCGGCAACGGCTACCGGCTGC	240
Db	302	GGAGGGGGGCAAGGACGTAAGTGTGTGTATAGTGTGAGCCGGCAACGGCTACCGGCTGC	361
Qy	241	AACGCCAAGCGGCTTCAAGCCCTGGGAGTGCNAACCGCGCCGCAACCGCCGCAAGCC	300
Db	362	AACGCCAAGCGGCTTCAAGCCCTGGGAGTGCNAACCGCGCCGCAACCGCCGCAAGCC	421
Qy	301	ATCAAGTTCTCGGAAAGTTCCAGCGCTACAGCGCTTCTCTGGGGCTACGAGTTCCAC	360
Db	422	ATCAAGTTCTCGGAAAGTTCCAGCGCTACAGCGCTTCTCTGGGGCTACGAGTTCCAC	481
Qy	361	GCCGGCCCAAGGACGTAATCTCTGACGCCCACTCAAACTTGCATCTGGAAGTCTCTG	420
Db	482	GCCGGCCCAAGGACGTAATCTCTGACGCCCACTCAAACTTGCATCTGGAAGTCTCTG	541
Qy	421	AGGATGAAGGTGTTGCTGCTGCGCCCTCCACATGCGACTCCGGGGGGAAGCCGGTCCC	480
Db	542	AGGATGAAGGTGTTGCTGCTGCGCCCTCCACATGCGACTCCGGGGGGAAGCCGGTCCC	601
Qy	481	ACTCTCCCGCAGTTTCCATGAGGCCCCCAATGTGAAGATCAAGGTGTGAAGACTTTGAG	540
Db	602	ACTCTCCCGCAGTTTCCATGAGGCCCCCAATGTGAAGATCAAGGTGTGAAGACTTTGAG	661
Qy	541	GGAGAAACCCCTAAGTGGCCCAAGCTTGAAGAAGATGACGGGGACCAAGCCCAAAACGG	600
Db	662	GGAGAAACCCCTAAGTGGCCCAAGCTTGAAGAAGATGACGGGGACCAAGCCCAAAACGG	721
Qy	601	GAACACCTGCGCCCTGGCCGCTGGGCAATGCGCTTCTTCTTCAATGAGCTTGGGCTCC	657
Db	722	GAACACCTGCGCCCTGGCCGCTGGGCAATGCGCTTCTTCTTCAATGAGCTTGGGCTCC	778

RESULT 2
 EX419695
 LOCUS
 DEFINITION BX419695 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 ACCESSION BX419695.2 GI:46934231
 VERSION EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (Bases 1 to 871)
 11, W.B., Gruber, C., Jesse, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT
 On May 13, 2003 this sequence version replaced gi:30654816.
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 497.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DF019D120P1&c=497.f.

FEATURES
 source
 1..871
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF019YB24"
 /issue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized."

Query Match
 Best Local Similarity 98.2%; Score 645; DB 5; Length 871;
 Matches 656; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CTGCTGCCCAAGGGCCCGGAGGGGGCGGTGGGAAAACCGGCATGCGGTGTAATGGAACAGC 60
 DB 114 CTGCTGCCCAAGGGCCCGGAGGGGGCGGTGGGAAAACCGGCATGCGGTGTAATGGAACAGC 60
 QY 61 TCCAACCAAGCCTTCCGGCCGAGAGGGGCTACACCGCTGCAAGTGAACGACTATCTCG 120
 DB 173 TCCAACCAAGCCTTCCGGCCGAGAGGGGCTACACCGCTGCAAGTGAACGACTATCTCG 120
 QY 121 GATATTTTACGCGCCGCACTAACAGCTCGGGGGTGGGCCCCCGGGGGGGAGACCGGGGCC 232
 DB 233 GATATTTTACGCGCCGCACTAACAGCTCGGGGGTGGGCCCCCGGGGGGGAGACCGGGGCC 232
 QY 181 GGAGGGGGGGGAGAGCAGTACGCTGTATGATGATGATGATGATGATGATGATGATGATGAT 292
 DB 293 GGAGGGGGGGGAGAGCAGTACGCTGTATGATGATGATGATGATGATGATGATGATGATGAT 292
 QY 241 AAGGCCAGCAGAGGGGTTGAAAGCGTGGAGATGAAACCGGCGGACCGCCGCAACAGCC 352
 DB 353 AAGGCCAGCAGAGGGGTTGAAAGCGTGGAGATGAAACCGGCGGACCGCCGCAACAGCC 352
 QY 301 ATCAAGTTCTGCGGAGAGTTCCAGCGCTTCTCTGAGCTGCAAGTCCAC 412
 DB 360 ATCAAGTTCTGCGGAGAGTTCCAGCGCTTCTCTGAGCTGCAAGTCCAC 412

DB 413 ATCAAGTTCTGCGGAGAGTTCCAGCGCTTCTCTGAGCTGCAAGTCCAC 412
 QY 361 GCCGGCCGAGATCTACTACATCTCCAGCCCACTCAACACTGCACTGCAAGTGTCTG 472
 DB 473 GCCGGCCGAGATCTACTACATCTCCAGCCCACTCAACACTGCACTGCAAGTGTCTG 472
 QY 421 AGATGAAAGTG 532
 DB 533 AGATGAAAGTG 532
 QY 481 ACTTCCCGCCAGTATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 593 ACTTCCCGCCAGTATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 592
 QY 541 GGAGGAAACCTCTGAGTGGCCCAAGCTTGGAGAGAGATCAGCCGGGAGAGCCGTTGAG 652
 DB 653 GGAGGAAACCTCTGAGTGGCCCAAGCTTGGAGAGAGATCAGCCGGGAGAGCCGTTGAG 652
 QY 601 GAACACCTGCTCCCTGCGTGGGCAATGCGCTTCTCTGATGAGCTTGGCTCC 657
 DB 713 GAACACCTGCTCCCTGCGTGGGCAATGCGCTTCTCTGATGAGCTTGGCTCC 657

RESULT 3
 AL533153
 LOCUS
 DEFINITION AL533153 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 ACCESSION AL533153
 VERSION AL533153.3 GI:45708058
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (Bases 1 to 1100)
 11, W.B., Gruber, C., Jesse, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT
 On Feb 13, 2001 this sequence version replaced gi:31070985.
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 497.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DN003CF10QPI&c=497.f.

FEATURES
 source
 1..1100
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DN003YI19"
 /issue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_lib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized."

Query Match
 Best Local Similarity 94.8%; Score 622.6; DB 1; Length 1100;
 Matches 655; Conservative 1; Mismatches 0; Indels 3; Gaps 3;

QY 1 CTGCTGCCCAAGGGCCCGGAGGGGGCGGTGGGAAAACCGGCATGCGGTGTAATGGAACAGC 60

Db 122 CTGCTGGCCCAAGAGGCGCCGGA-GGGCGCTGGGAAAACCGGCATGGGTGTATGGAAACAGC 180
 Qy 61 TCACAACGACGACCTTGGGGCCGAGAGGGCTTACACCGTGTGAGTGAACCTGTAATCTGTG 120
 Db 181 TCCAACACGACGACCTTGGGGCCGAGAGGGCTTACACCGTGTGAGTGAACCTGTAATCTGTG 240
 Qy 121 GATATTACTGCGCCGCACTACAAAGGCTGGGGGGTGGGGCCCGGGGGGGGGGGGGGGGGGGCC 180
 Db 241 GATATTACTGCGCCGCACTACAAAGGCTGGGGGGTGGGGCCCGGGGGGGGGGGGGGGGGGGCC 300
 Qy 181 GGAAGCGGGGAGAGGAGTACGCTGTGTACATGGTGTGAGCGCCGCAACCGCTACCGGCACTGTG 240
 Db 301 GGAAGCGGGGAGAGGAGTACGCTGTGTACATGGTGTGAGCGCCGCAACCGCTACCGGCACTGTG 360
 Qy 241 AAGCGCCGCAAGGGGCTTCAAGCGCTGGGAGTGCACCGGCGCCGCAACCGGCGCCGCAAGCGCC 300
 Db 361 AAGCGCCGCAAGGGGCTTCAAGCGCTGGGAGTGCACCGGCGCCGCAACCGGCGCCGCAAGCGCC 420
 Qy 301 ATCAAGTTCTCCGGAAGGTTCCAGCGCTTACAGCGCGCTTCTCTT-GGGCTACCGAGTTCCA 359
 Db 421 ATCAAGTTCTCCGGAAGGTTCCAGCGCTTACAGCGCGCTTCTCTTGGGGGTACGAGTTCCA 480
 Qy 360 CGCGCGCCAGAGTACTATCATCTCCAGCGCCGCACTACAACTGTGCACTGGAAAGTGTCT 419
 Db 481 CGCGCGCCAGAGTACTATCATCTCCAGCGCCGCACTACAACTGTGCACTGGAAAGTGTCT 540
 Qy 420 GAGGATGAGGAGTGTCTGCTGTGCTGGCGCTCCAGATGCGGCACTCC-GGGGAGAAAGCGGCTCC 478
 Db 541 GAGGATGAGGAGTGTCTGCTGTGCTGGCGCTCCAGATGCGGCACTCCGGGGGAGAAAGCGGCTCC 600
 Qy 479 CCACTCTCCCGCCAGTTCCACATGGGGCCCGCAATGTGAAGATCAAGGTGTGGAAACCTTTGG 538
 Db 601 CCACTCTCCCGCCAGTTCCACATGGGGCCCGCAATGTGAAGATCAAGGTGTGGAAACCTTTGG 660
 Qy 539 AGGAGAGAAACCTTCAGAGTGGCCCAAGCTTGAAGAGAGATCAGGCGGGGCAACCGCCCAAC 598
 Db 661 AGGAGAGAAACCTTCAGAGTGGCCCAAGCTTGAAGAGAGATCAGGCGGGGCAACCGCCCAAC 720
 Qy 599 GGGAAACACTGCTGCCCTGGCGTGGGAGTCCGCTTCTTCTGTGATGAGCTTTTGGCCCTCC 657
 Db 721 GGGAAACACTGCTGCCCTGGCGTGGGAGTCCGCTTCTTCTGTGATGAGCTTTTGGCCCTCC 779

RESULT 4
 AL527972 726 bp mRNA linear EST 24-MAR-2004
 LOCUS AL527972 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cdna clone CS0DC027YPI9 5-PRIME, mRNA sequence.
 ACCESSION AL527972 GI:45703058
 VERSION AL527972.3
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 726)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 13, 2001 this sequence version replaced gi:31065823.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 497.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdnats=CS0DC027CHI0QPl&c=497.f.

FEATURES
 source Location/Qualifiers
 1..726 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC027YPI9"
 /issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 91.1%; Score 598.4; DB 1; Length 726;
 BeSt Local Similarity 91.0%; Pred. No. 2,8e-129;
 Matches 595; Conservative 41; Mismatches 17; Indels 1; Gaps 1;

1 CTGCTGGCCCAAGAGGCGCCGGA-GGGCGCTGGGAAAACCGGCATGGGTGTATGGAAACAGC 60
 Db 69 CTGCTGGCCCAAGAGGCGCCGGA-GGGCGAAGGAAAACMGGCATGGGTGTATGGAAACAGC 127
 Qy 61 TCACAACGACGACCTTGGGGCCGAGAGGGCTTACACCGTGTGAGTGAACCTGTAATCTGTG 120
 Db 128 WCAACACGACGACCTTGGGGCCGAGAGGGCTTACACCGTGTGAGTGAACCTGTAATCTGTG 187
 Qy 121 GATATTACTGCGCCGCACTACAAAGGCTGGGGGGTGGGGCCCGGGGGGGGGGGGGGGGGGGCC 180
 Db 188 GATATMMWAAAAGCAGMAMTAAAAMAGMCGGGGGTGGGGCCCGGGGGGGGGGGGGGGGGGGCC 247
 Qy 181 GGAAGCGGGGAGAGGAGTACGCTGTGTACATGGTGTGAGCGCCGCAACCGCTACCGGCACTGTG 240
 Db 248 GGAAGCGGGGAGAGGAGTACGCTGTGTACATGGTGTGAGCGCCGCAACCGCTACCGGCACTGTG 307
 Qy 241 AAGCGCCGCAAGGGGCTTCAAGCGCTGGGAGTGCACCGGCGCCGCAACCGGCGCCGCAAGCGCC 300
 Db 308 AAGCGCCGCAAGGGGCTTMAAGCGCTGGGAGTGCACCGGCGCCGCAACCGGCGCCGCAAGCGCC 367
 Qy 301 ATCAAGTTCTCCGGAAGGTTCCAGCGCTTACAGCGCGCTTCTCTTGGGGGTACGAGTTCCAC 360
 Db 368 ATMAAGTTCTCCGGAAGGTTCCAGCGCGCTTCTCTTGGGGGTACGAGTTCCAC 427
 Qy 361 GCGGGCCAGAGTACTATCATCTCCAGCGCCGCACTACAACTGTGCACTGGAAAGTGTCTG 420
 Db 428 CWMGGCCAGAGTACTATCATCTCCAGCGCCGCACTACAACTGTGCACTGGAAAGTGTCTG 487
 Qy 421 AGGATGAGGAGTGTCTGCTGTGCTGGCGCTCCAGATGCGGCACTCCGGGGAGAAAGCGGCTCCC 480
 Db 488 ARGATGAGGAGTGTCTGCTGTGCTGGCGCTCCAGATGCGGCACTCCGGGGAGAAAGCGGCTCCC 547
 Qy 481 ACTGTCCCGCAGATTACCAATGGGCGCCCAAGTGTGAAGATCAACGTTCTGTTGAAAGACTTTGAG 540
 Db 548 ACTGTCCCGCAGATTACCAATGGGCGCCCAAGTGTGAAGATCAACGTTCTGTTGAAAGACTTTGAG 607
 Qy 541 GGAAGAAACCTTCAAGGAGCCCAAGCTTGAAGAGATCAGGCGGGGAAACCGCCCAACCGG 600
 Db 608 GGAAGAAACCTTCAAGGAGCCCAAGCTTGAAGAGATCAGGCGGGGAAACCGCCCAACCGG 667
 Qy 601 GAACACCTTGGCCCTGGCGGAGTCCGCTTCTTCTGATGAGCTTTTGGCC 654
 Db 668 GAACACCTTGGCCCTGGCGGAGTCCGCTTCTTCTGATGAGCTTTTGGCC 721

RESULT 5
 CRS97504 1629 bp mRNA linear HTC 21-JUN-2004
 LOCUS CRS97504
 DEFINITION full-length cDNA clone GS0D1026Y124 of Placenta Cot 25-normalized
 of Homo sapiens (human).
 ACCESSION CRS97504
 VERSION CRS97504.1 GI:50478311
 KEYWORDS HTC; CNSLT cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS 1 (bases 1 to 1629)
 TITLE Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 JOURNAL Full-length cDNA libraries and normalization
 REMARK Unpublished
 Contact: Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Paraday Avenue
 2 (bases 1 to 1629)
 Genoscope.
 Direct Submission
 Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage:
 BP 191 91006 Evry cedex - FRANCE (E-mail: segre@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 Location/Qualifiers
 1. 1629

COMMENT /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CGSOD1026Y124"
 /issue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

FEATURES
 source
 Location/Qualifiers
 1. 1629

ORIGIN

Query Match
 Best Local Similarity 89.4%; Score 587.2; DB 3; Length 1629;
 Matches 589; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

66 CCACGACCTCGCGCGGAGAGGGCTTACACCGTGCAGGTGAAACGTGACACTATCTGATAT
 77 CCAAGCTCGCGCGGAGAGGGCTTACACCGTGCAGGTGAAACGTGACACTATCTGATAT
 126 TTAAGTCCCGGCACTACAAAGCTCGGGGAGTGGCCCGGGGGGGGACCGGGGGGGGGG
 137 TTAAGTCCCGGCACTACAAAGCTCGGGGAGTGGCCCGGGGGGGGACCGGGGGGGGGG
 186 CCGGGCAGAGGAGTACGCTGTGATCAATGTGTGAGCCGCAACGGCTACCGCACTGCAACCC
 197 CCGGGCAGAGGAGTACGCTGTGATCAATGTGTGAGCCGCAACGGCTACCGCACTGCAACCC
 246 CAGCCAGGCGCTTCAAGGCGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
 257 CAGCCAGGCGCTTCAAGGCGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
 306 GTTCTGGAGAAAGTTCAGCCGCTAAGGCGCTTCTCTGTGGGCTAGAGTTTCACGCCGG
 317 GTTCTGGAGAAAGTTCAGCCGCTAAGGCGCTTCTCTGTGGGCTAAGGCGCTTCTCTGTGGG
 366 CCAAGGAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT
 377 CCAAGGAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT
 426 GAAAGTGTGCTGTGCTGCGCCTCAATCGACTCCGGGGAGAAAGCCGGTCCCACTCT
 437 GAAAGTGTGCTGTGCTGCGCCTCAATCGACTCCGGGGAGAAAGCCGGTCCCACTCT
 486 CCGCCAGTTACCCATGGGCCCAATGTAAGATCAACGTCGTGAAAGACTTTGAGGGAGA
 497 CCGCCAGTTACCCATGGGCCCAATGTAAGATCAACGTCGTGAAAGACTTTGAGGGAGA
 546 GAAACCTCAGTGTGCCCAAGCTTGAAGAGAGCATCAGGGGAGCAAGCCCAAAACGGGAACA
 557 GAAACCTCAGTGTGCCCAAGCTTGAAGAGAGCATCAGGGGAGCAAGCCCAAAACGGGAACA
 606 CTTGCCCTGGCGGTTGGGCAATCGCCTTCTTCTCATGAGCTTTTGGCCTCC 657
 617 CTTGCCCTGGCGGTTGGGCAATCGCCTTCTTCTCATGAGCTTTTGGCCTCC 668

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 09:30:04 ; Search time 3083.91 Seconds
(without alignments)
8183.329 Million cell updates/sec

Title: US-09-904-954-1_COPY_83_745
Perfect score: 663
Sequence: 1 ATGGCGGGCGGCTCCGGTGC...CCAGCCCAAAAGGAAACAC 663

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Libring first 1500 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hnc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	100.0	1741	CR607482	full-length
2	651	98.2	871	BX419695	BX419695
3	628.6	94.8	1100	AL533153	AL533153
4	603.8	91.1	726	AL527972	AL527972

ALIGNMENTS

RESULT 1
CR607482
LOCUS: CR607482 1741 bp mRNA linear HTC 21-JUL-2004
DEFINITION: full-length cDNA clone CSODN003YL19 of Adult Brain of Homo sapiens (human).
ACCESSION: CR607482
VERSION: CR607482.1 GI:50488289
KEYWORDS: HTC; CNSLT cDNA.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1741)
AUTHORS: Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
TITLE: Full-length cDNA libraries and normalization

JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/InvitrogenCorporation1600FaradayAvenue2(Bases1to1741)

REFERENCE JOURNAL Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
AUTHORS BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

COMMENT

Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime ends enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source
Location/Qualifiers
1..1741
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN003YL19"
/issue_type="Adult brain"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 100.0%; Score 663; DB 3; Length 1741;
Best Local Similarity 100.0%; Pred. No. 6.4e-137; Indels 0; Gaps 0;

Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65																																																																	
QY	DB	1	ATGGCGGGCGGCTCCGGTGC	2	CGGCTCCGGTGC	3	CGGCTCCGGTGC	4	CGGCTCCGGTGC	5	CGGCTCCGGTGC	6	CGGCTCCGGTGC	7	CGGCTCCGGTGC	8	CGGCTCCGGTGC	9	CGGCTCCGGTGC	10	CGGCTCCGGTGC	11	CGGCTCCGGTGC	12	CGGCTCCGGTGC	13	CGGCTCCGGTGC	14	CGGCTCCGGTGC	15	CGGCTCCGGTGC	16	CGGCTCCGGTGC	17	CGGCTCCGGTGC	18	CGGCTCCGGTGC	19	CGGCTCCGGTGC	20	CGGCTCCGGTGC	21	CGGCTCCGGTGC	22	CGGCTCCGGTGC	23	CGGCTCCGGTGC	24	CGGCTCCGGTGC	25	CGGCTCCGGTGC	26	CGGCTCCGGTGC	27	CGGCTCCGGTGC	28	CGGCTCCGGTGC	29	CGGCTCCGGTGC	30	CGGCTCCGGTGC	31	CGGCTCCGGTGC	32	CGGCTCCGGTGC	33	CGGCTCCGGTGC	34	CGGCTCCGGTGC	35	CGGCTCCGGTGC	36	CGGCTCCGGTGC	37	CGGCTCCGGTGC	38	CGGCTCCGGTGC	39	CGGCTCCGGTGC	40	CGGCTCCGGTGC	41	CGGCTCCGGTGC	42	CGGCTCCGGTGC	43	CGGCTCCGGTGC	44	CGGCTCCGGTGC	45	CGGCTCCGGTGC	46	CGGCTCCGGTGC	47	CGGCTCCGGTGC	48	CGGCTCCGGTGC	49	CGGCTCCGGTGC	50	CGGCTCCGGTGC	51	CGGCTCCGGTGC	52	CGGCTCCGGTGC	53	CGGCTCCGGTGC	54	CGGCTCCGGTGC	55	CGGCTCCGGTGC	56	CGGCTCCGGTGC	57	CGGCTCCGGTGC	58	CGGCTCCGGTGC	59	CGGCTCCGGTGC	60	CGGCTCCGGTGC	61	CGGCTCCGGTGC	62	CGGCTCCGGTGC	63	CGGCTCCGGTGC	64	CGGCTCCGGTGC	65	CGGCTCCGGTGC

ORIGIN

Query Match 94.8%; Score 628.6; DB 1; Length 1100; Best Local Similarity 99.4%; Pred. No. 2,7e-129; Matches 661; Conservative 1; Mismatches 0; Indels 3; Gaps 3;

Table with columns: QY, Db, Accession, and sequence alignment. It shows a high degree of similarity between the query and database sequences, with a score of 628.6.

RESULT 4 AL527972 726 bp mRNA linear EST 24-MAR-2004

LOCUS AL527972 Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED Homo sapiens DEFINITION cDNA clone CS0DC027YP19 5-PRIME, mRNA sequence.

ACCESSION AL527972 GI:45703058 VERSION 1 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 726) Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo. AUTHORS Li, W.B., Guber, C., Jessee, J. and Polayes, D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT On Feb 13, 2001 this sequence version replaced gi:31065823. Contact: Genoscope

Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

FEATURES source /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DC027YP19" /issue_type="NEUROBLASTOMA COR 25-NORMALIZED" /clone_lib="Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN Query Match 91.1%; Score 603.8; DB 1; Length 726; Best Local Similarity 89.0%; Pred. No. 8.6e-124; Matches 590; Conservative 48; Mismatches 25; Indels 0; Gaps 0;

Table with columns: QY, Db, Accession, and sequence alignment. It shows a high degree of similarity between the query and database sequences, with a score of 603.8.

Wed Apr 20 07:32:03 2005

QY 661 CAC 663
DB 671 CAC 673

Search completed: April 19, 2005, 21:57:07
Job time : 3085.05 secs

us-09-904-954-1_copy_83_745.rst

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2005, 15:35:11 ; Search time 59.9368 Seconds
(without alignments)
1413.163 Million cell updates/sec

Title: US-09-904-954-2_COPY_1_219

Perfect score: 1207
Sequence: 1 MAAAPLILLLLVVPLPLP.....GNNPQVPLKELKISIGTSFKR 219

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing first 1500 summaries

- Database :
- 1: A_Geneseq_16Dec04:*
 - 2: geneseqp1980s:*
 - 3: geneseqp1990s:*
 - 4: geneseqp2000s:*
 - 5: geneseqp2001s:*
 - 6: geneseqp2002s:*
 - 7: geneseqp2003as:*
 - 8: geneseqp2003bs:*
 - 9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1207	100.0	238	AA71481	Human hek
2	1207	100.0	238	AA79439	Breast/co
3	1207	100.0	238	ADP97190	Tumour/as
4	1207	100.0	238	Adh38812	Cancer/an
5	1207	100.0	238	Adq21666	Human sof
6	1172	97.1	234	AA82605	Eph trans

ALIGNMENTS

RESULT 1
ID AAR71481 standard; protein; 238 AA.

AA71481; AAR71481; 25-MAR-2003 (revised) 03-OCT-1995 (first entry) Human hek-L protein. Ligand; cell surface; tyrosine kinase receptor; tumorigenesis; immunogen. Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..19
FT /note="signal peptide"
FT Protein 20..238

XX MO9506065-A1.

XX 02-MAR-1995.

XX 17-AUG-1994; 94MO-US009282.

XX 20-AUG-1993; 93US-00109745.

XX 30-AUG-1993; 93US-00114426.

XX 03-DEC-1993; 93US-00161132.

XX 09-MAY-1994; 94US-00240124.

XX (IMMV) IMMUNEX CORP.

XX Beckmann MP, Cerretti DP;

XX WPI; 1995-106811/14.

XX N-PSDB; AA085887.

XX New isolated DNA encoding hek-L protein or its fusion products - useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukemia cells.

XX Claim 21; Page 36; 45pp; English.

The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors. See also AAR71482. (Updated on 25-MAR-2003 to correct PN field.)

Query Match 100.0%; Score 1207; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.8e-115;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAAAPLILLLLVVPLPLPILAAQPGGALGNRHAVVYVNSNQHARRREGYTVQVNVNDYLD	60
Db	1	MAAAPLILLLLVVPLPLPILAAQPGGALGNRHAVVYVNSNQHARRREGYTVQVNVNDYLD	60
Qy	61	IYCPHYNSVGVGPGAGPGGAEQYVLYVNSVNGYRTCNASQGFYRWECNRPDHPHSP1	120
Db	61	IYCPHYNSVGVGPGAGPGGAEQYVLYVNSVNGYRTCNASQGFYRWECNRPDHPHSP1	120
Qy	121	KESEKQRYSAESLGYEFAHGHYYIYIPTTHLHMKCLRMKRVNCCASVSHGKRPVPT	180
Db	121	KESEKQRYSAESLGYEFAHGHYYIYIPTTHLHMKCLRMKRVNCCASVSHGKRPVPT	180
Qy	121	KFSEKQRYSAESLGYEFAHGHYYIYIPTTHLHMKCLRMKRVNCCASVSHGKRPVPT	180
Db	121	KFSEKQRYSAESLGYEFAHGHYYIYIPTTHLHMKCLRMKRVNCCASVSHGKRPVPT	180
Qy	181	LPQFTMGPNVKNVLESDPFGENPQVPLKELKISIGTSFKR 219	
Db	181	LPQFTMGPNVKNVLESDPFGENPQVPLKELKISIGTSFKR 219	

RESULT 2
ID AAG79439 standard; protein; 238 AA.

AA79439; AAG79439; 25-OCT-2002 (first entry) Breast/colon cancer associated protein.

XX Breast; colon; cancer; diagnosis; colorectal; prognosis; gene therapy;
 KW CHA4; CBK8.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 6..238 /note="Encoded by ABA00091"
 PN WO2002595609-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 10-DEC-2001; 2001WO-US048358.
 PR 08-DEC-2000; 2000US-00733756.
 XX 08-DEC-2000; 2000US-00733757.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 PI Mack DH, Gish KC, Wilson KE;
 XX WPI; 2002-595815/64.
 DR N-PSDB; ABA00091.
 XX
 PT Diagnosing cancer by determining the expression profile gene that encodes
 the CHA4 or CBK8 protein, useful for the treatment and prognosis of
 breast and colorectal cancer.
 XX
 PS Disclosure; Fig 2; 95pp; English.
 XX
 CC The sequences given in ABA00086-92 represent sequences which have been
 associated with either breast and/or colon cancer. These sequences may be
 used in the method of the invention for diagnosing cancer. The method
 comprises determining the expression of one or more specified genes in a
 colorectal tissue sample, or in a breast tissue sample of a first
 individual. The method of the invention is useful for the diagnosis,
 treatment and prognosis of breast and/or colorectal cancer. The invention
 also provides for methods useful for modulating activity and inhibiting
 breast and/or colorectal cancer. Prior methods of diagnosing and
 prognosticating breast and colorectal cancer have been limited and
 problematic. The present methods of gene therapy using novel sequences
 for the diagnosis and prognosis of cancer including screening for drug
 candidates and bioactive agents that modulates CHA4 or CBK8, makes their
 use and purpose limitless and more specific especially in the area of
 grading prognostic factors. This sequence represents CHA4 which has the
 bioactivity of a breast cancer modulating protein
 CC
 CC Sequence 238 AA;
 XX

ABP97190
 ID ABP97190 standard; protein; 238 AA.
 XX
 AC ABP97190;
 XX
 DT 01-JUL-2003 (first entry)
 DE Tumour-associated antigenic target protein TAT178 SEQ ID NO:72.
 KW Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
 XX cancer.
 XX Homo sapiens.
 OS
 XX
 PN NO2003024392-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 11-SEP-2002; 2002NO-US028859.
 PR 18-SEP-2001; 2001US-0323268P.
 XX 19-OCT-2001; 2001US-0339227P.
 PR 07-NOV-2001; 2001US-0336827P.
 XX 20-NOV-2001; 2001US-0331906P.
 PR 02-JAN-2002; 2002US-0345444P.
 XX 03-APR-2002; 2002US-0369724P.
 PR 19-AUG-2002; 2002US-0404809P.
 XX
 PA (GETH) GENENTECH INC.
 PI
 PI Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;
 XX Williams PM, Wu TD, Zhang Z;
 XX WPI; 2003-354551/33.
 DR N-PSDB; ACC49508.
 XX
 PT New antibodies against tumor-associated antigenic target polypeptide,
 useful for treating or diagnosing tumors or cancers in mammals, e.g.
 prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
 carcinomas.
 XX
 PS Claim 2; Fig 72; 285pp; English.
 XX
 CC ACC49493 to ACC49552 encode the human tumour-associated antigenic target
 CC (TAT) proteins given in ABP97175 to ABP97234. The present invention
 CC describes an isolated antibody that binds to a polypeptide having at
 CC least 80 % sequence identity to any of the 60 150-800 residue amino acid
 CC sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
 CC its associated signal peptide, encoded by any of the 60 2000-3000 base
 CC cytosolic actvity. The antibody can be used for treating or diagnosing
 CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
 CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
 CC cell carcinomas, or thyroid cancer
 XX
 XX Sequence 238 AA;
 XX

Query Match
 Best Local Similarity 100.0%; Score 1207; DB 5; Length 238;
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
 Best Local Similarity 100.0%; Score 1207; DB 6; Length 238;
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MAAAPLILLLLVVPLPLLAQGGALGNRRHAYVWVSSNQHLLRREGYTVQVWVNDYLD 60
 QY IYCPHYNSSGVGPGAGGPGGGAEOYVLYVWSRNGYRTCAASQGFKRWEBCNRPHAHSPFI 120
 Db 61 IYCPHYNSSGVGPGAGGPGGGAEOYVLYVWSRNGYRTCAASQGFKRWEBCNRPHAHSPFI 120
 QY IYCPHYNSSGVGPGAGGPGGGAEOYVLYVWSRNGYRTCAASQGFKRWEBCNRPHAHSPFI 120
 Db 121 KFSEKFORYSASFSLGYEFHAGHEYYIISTPTHNLHMVKCLRMKVFVCCASTSHSGEKVPPT 180
 QY KFSEKFORYSASFSLGYEFHAGHEYYIISTPTHNLHMVKCLRMKVFVCCASTSHSGEKVPPT 180
 Db 181 LPOFTWGPVWKTINVLDEDEGENPOVPLKLEKISIGSTSPKR 219
 QY LPOFTWGPVWKTINVLDEDEGENPOVPLKLEKISIGSTSPKR 219
 Db 181 LPOFTWGPVWKTINVLDEDEGENPOVPLKLEKISIGSTSPKR 219

Db 1 MAAAPLILLLLVVPLPLLAQGGALGNRRHAYVWVSSNQHLLRREGYTVQVWVNDYLD 60
 QY IYCPHYNSSGVGPGAGGPGGGAEOYVLYVWSRNGYRTCAASQGFKRWEBCNRPHAHSPFI 120
 Db 61 IYCPHYNSSGVGPGAGGPGGGAEOYVLYVWSRNGYRTCAASQGFKRWEBCNRPHAHSPFI 120
 QY IYCPHYNSSGVGPGAGGPGGGAEOYVLYVWSRNGYRTCAASQGFKRWEBCNRPHAHSPFI 120
 Db 121 KFSEKFORYSASFSLGYEFHAGHEYYIISTPTHNLHMVKCLRMKVFVCCASTSHSGEKVPPT 180
 QY KFSEKFORYSASFSLGYEFHAGHEYYIISTPTHNLHMVKCLRMKVFVCCASTSHSGEKVPPT 180
 Db 181 LPOFTWGPVWKTINVLDEDEGENPOVPLKLEKISIGSTSPKR 219

RESULT 3

OY 181 LPQFTMGPNVKINVLDEPGEENPQVPLKESISGTSRPR 219
DB 181 LPQFTMGPNVKINVLDEPGEENPQVPLKESISGTSRPR 219

RESULT 4
ADN38812 standard; protein; 238 AA.
ADN38812: ADN38812:

DT 17-JUN-2004 (first entry)
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:130.

KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnetary; gene therapy; vaccine.

OS Homo sapiens.
XX MO2003042661-A2.

PD 22-MAY-2003.
XX 13-NOV-2002; 2002MO-US036810.

PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0352525P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386644P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glyne R, Hevezl PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
XX WPI; 2003-468649/44.
DR N-SDSB; ADN38811.

XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO 130; 1385bp; English.

CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;

CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis; inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.

SO Sequence 238 AA:
Query Match 100.0%; Score 1207; DB 7; Length 238;
Best Local Similarity 100.0%; Pred. No. 1,8e-115;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAAAPLLLLLIVVPLPLPILAAQGGALNRRHVVWVWVNSNOHRRRGYTVQVWVNYLD 60
DB 1 MAAAPLLLLLIVVPLPLPILAAQGGALNRRHVVWVWVNSNOHRRRGYTVQVWVNYLD 60
OY 61 IYCPHYNSGIVGAGGPGGGAEGQVYLVVWSRNGYRTCNASOGFKMECNRPAPHSPI 120
DB 61 IYCPHYNSGIVGAGGPGGGAEGQVYLVVWSRNGYRTCNASOGFKMECNRPAPHSPI 120

OY 121 KFSKRFQRYSAFSLGVEFHAHEYYIISTPTHNLHMKVLPVCCASTSHSGEKEVPT 180
DB 121 KFSKRFQRYSAFSLGVEFHAHEYYIISTPTHNLHMKVLPVCCASTSHSGEKEVPT 180

OY 181 LPQFTMGPNVKINVLDEPGEENPQVPLKESISGTSRPR 219
DB 181 LPQFTMGPNVKINVLDEPGEENPQVPLKESISGTSRPR 219

RESULT 5
ADQ21666 standard; protein; 238 AA.
ADQ21666:

XX 26-AUG-2004 (first entry)
XX Human soft tissue sarcoma-upregulated; protein - SEQ ID 4486.
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
OS Homo sapiens.
XX MO2004048938-A2.
XX 10-JUN-2004.
XX 26-NOV-2003; 2003MO-US038193.
XX 26-NOV-2002; 2002US-0429739P.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Aziz N, Ginsburg WM, Zlotnick A;
XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.

XX Example 2; SEQ ID NO 4486; 210pp; English.

CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the

CC Presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX Sequence 238 AA;

Query Match
 Best Local Similarity 100.0%; Score 1207; DB 8; Length 238;
 Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPPLLLLLVLPVPLPILLAQGGGALGNRHAVYVWNSNQHRRREGYTVQVWVNDYLD 60
 Db 1 MAAPPLLLLLVLPVPLPILLAQGGGALGNRHAVYVWNSNQHRRREGYTVQVWVNDYLD 60
 QY 61 IYCPHYNSGGVGGPGRGGGAEQYVLYVWVSRNGYRTCNASOGFRWRWCNRPHAPHSPI 120
 Db 61 IYCPHYNSGGVGGPGRGGGAEQYVLYVWVSRNGYRTCNASOGFRWRWCNRPHAPHSPI 120
 QY 121 KFESEKFORYSARFSLGYEFHAGHEYYIISTPTNHLHWKCLRMRKVFVCCASTSHSGEKVPT 120
 Db 121 KFESEKFORYSARFSLGYEFHAGHEYYIISTPTNHLHWKCLRMRKVFVCCASTSHSGEKVPT 120
 QY 181 LPOFTMGPNVXKINVLDEDFEGENPOVPRKLEKSIIGTSPKR 219
 Db 181 LPOFTMGPNVXKINVLDEDFEGENPOVPRKLEKSIIGTSPKR 219

RESULT 6
 AAR82605
 ID AAR82605 standard; protein; 234 AA.
 AC AAR82605;
 XX
 DT 16-MAY-1996 (first entry)
 DE Eph transmembrane tyrosine kinase family ligand, Efl-2.
 KW Efl-2; EHKL1; Eph transmembrane tyrosine kinase family ligand.
 KM neurological disorder; identification; diagnosis.
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..30 Location/Qualifiers
 FT Misc-difference 158 /label= signal_peptide
 FT Region /note= "residue borders main conserved regions"
 FT 218..235 /note= "carboxy terminal hydrophobic GPI-recognition
 tail"
 XX
 EN W09527060-A2.
 PD 12-OCT-1995.
 XX
 PF 04-APR-1995; 95WO-US004208.
 XX
 PR 04-APR-1994; 94US-002224075.
 PR 12-APR-1994; 94US-002224075.
 PR 01-SEP-1994; 94US-002224072.
 PR 21-OCT-1994; 94US-00299567.
 XX
 PA (REG-) REGENERON PHARM INC.
 FI Davis S, Gale N, Aldrich TH, Maisompierre PC, Goldfarb M,
 FI Yancopoulos GD,
 FI
 DR WPI; 1995-358635/46.
 DR N-PSDB; AAT03883.

XX Ligands which bind Eph family receptors - used in the diagnosis of
 FT neurological disorders.
 PS Disclosure; Fig 2; 58pp; English.
 XX
 CC Efl-2 (also known as EHKL-1) is an Eph transmembrane tyrosine kinase
 CC family ligand. It has homology with B61 (Efl-1) (see AAR82604). Efl-2
 CC ends in a C-terminal hydrophobic sequence that appears to be a
 CC recognition sequence allowing it to be GPI-linked and thus lacking in an
 CC intracellular domain. Efl-2 is useful for identifying other ligands for
 CC EHKL-1, -2, -3, Eck and Elk receptors. The ligands are useful in promoting
 CC an and/or proliferative function and/or influencing the phenotype, such as growth
 CC diagnosis, and treatment of neurological disorders
 XX
 XX Sequence 234 AA;

Query Match
 Best Local Similarity 97.1%; Score 1172; DB 2; Length 234;
 Matches 215; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 MAAPPLLLLLVLPVPLPILLAQGGGALGNRHAVYVWNSNQHRRREGYTVQVWVNDYLD 60
 Db 1 MAAPPLLLLLVLPVPLPILLAQGGGALGNRHAVYVWNSNQHRRREGYTVQVWVNDYLD 60
 QY 61 IYCPHYNSGGVGGPGRGGGAEQYVLYVWVSRNGYRTCNASOGFRWRWCNRPHAPHSPI 120
 Db 61 IYCPHYNSGGVGGPGRGGGAEQYVLYVWVSRNGYRTCNASOGFRWRWCNRPHAPHSPI 120
 QY 121 KFESEKFORYSARFSLGYEFHAGHEYYIISTPTNHLHWKCLRMRKVFVCCASTSHSGEKVPT 116
 Db 121 KFESEKFORYSARFSLGYEFHAGHEYYIISTPTNHLHWKCLRMRKVFVCCASTSHSGEKVPT 116
 QY 181 LPOFTMGPNVXKINVLDEDFEGENPOVPRKLEKSIIGTSPKR 219
 Db 177 LPOFTMGPNVXKINVLDEDFEGENPOVPRKLEKSIIGTSPKR 215

Search completed: April 19, 2005, 23:13:33
 Job time : 59.9368 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 09:30:04 ; Search time 391.37 Seconds
(without alignments)
8258.620 Million cell updates/sec

Title: US-09-904-954-3_COPY_28_573

Perfect score: 546
Sequence: 1 ATGCGGGCTGCTGCCCCCTGCT.....GAGGGGGGAGCACTCCOAGC 546

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing first 1500 summaries

- Database :
- 1: N_Geneseq_16Dec04:**
 - 2: geneseqn1980s:**
 - 3: geneseqn1990s:**
 - 4: geneseqn2000s:**
 - 5: geneseqn2001as:**
 - 6: geneseqn2001bs:**
 - 7: geneseqn2002as:**
 - 8: geneseqn2002bs:**
 - 9: geneseqn2003as:**
 - 10: geneseqn2003bs:**
 - 11: geneseqn2003ds:**
 - 12: geneseqn2004as:**
 - 13: geneseqn2004bs:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	100.0	636	AAQ85888	AAG85888 Human hek
2	546	100.0	1181	ABZ34863	ABZ34863 Coding se
3	544.4	99.7	606	ABV78135	ABV78135 Human eph
4	544.4	99.7	606	ABZ35711	ABZ35711 Human eph
5	544.4	99.7	606	ABX09954	ABX09954 Human eph
6	544.4	99.7	606	ABL91676	ABL91676 Human pol

ALIGNMENTS

RESULT 1
AAQ85888
ID AAQ85888 standard; cDNA to mRNA; 636 BP.
XX
AC AAQ85888;
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-1995 (first entry)
XX

ID	Description	Location/Qualifiers
DE	Human hek-L protein cDNA clone C6.	
XX	Ligand; cell surface; tyrosine Kinase receptor; tumorigenesis; immunogen;	
KW	seq.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	28..633
FT	CDS	/*tag= a
FT	sig_peptide	28..93
FT	mat_peptide	/*tag= b
FT		94..630
FT		/*tag= c
XX		
PN	W09506065-A1.	
XX		
PD	02-MAR-1995.	
XX		
PF	17-AUG-1994; 94MO-US009282.	
XX		
PK	20-AUG-1993; 93US-00109745.	
PR	30-AUG-1993; 93US-00114426.	
PR	03-DEC-1993; 93US-00161132.	
PR	09-MAY-1994; 94US-00240124.	
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
PI	Beckmann MP, Cerretti DP;	
XX		
DR	WPI; 1995-106811/14.	
DR	P-PSDB; AAR71482.	
XX		
PT	New isolated DNA encoding hek-L protein or its fusion products - useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukemia cells.	
XX		
PS	Claim 3; Page 37; 45pp; English.	
XX		
CC	The sequence is that of a clone encoding hek-L protein, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors. See also AAQ85887. (Updated on 25-MAR-2003 to correct PN field.)	
XX		
SQ	Sequence 636 BP; 102 A; 202 C; 186 G; 146 T; 0 U; 0 Other;	
XX		
QY	Query Match	100.0%; Score 546; DB 2; Length 636;
	Best Local Similarity	100.0%; Pred. No. 2.1e-138;
	Matches	546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	61	CGGGGGGGCTCCAGCCCTCCGCGCAGTAGTACTAGGAACTCCAGTAAACCCAGGTTGCTT 120
Qy	61	
Db	88	CGGGGGGGCTCCAGCCCTCCGCGCAGTAGTACTAGGAACTCCAGTAAACCCAGGTTGCTT 147
Qy	88	
Db	121	CGAGAGACGCGCTGTGTGAGCTGGCCCTCAACGATTAAGTACATTTGTCTGCCCCAC 180
Qy	121	
Db	148	CGAGAGACGCGCGTGTGTGAGCTGGCCCTCAACGATTAAGTACATTTGTCTGCCCCAC 207
Qy	148	
Db	181	TACGAAGGCCAGGGCCCCCTGAGGGCCCCCGAAGACGTTTGCTTTGACATGTGTGACTGG 240
Qy	181	
Db	208	TACGAAGGCCAGGGCCCCCTGAGGGCCCCCGAAGACGTTTGCTTTGACATGTGTGACTGG 267
Qy	208	
Db	241	CCAGGCTATGATGCTCTGCCAGGAGGGCCCCCGGAGCTTACAAAGCGCTGGTGTCTCC 300
Qy	241	

PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.

PS Claim 10, Page 123, 203pp; German.

CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (ds1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention

XX Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other;

XX Query Match 99.7%; Score 544.4; DB 6; Length 606;

XX Best Local Similarity 99.8%; Pred. No. 5.5e-138;

XX Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGGCTGCTGCGCCCGCTGCGGACGTCCCTCGGGCCGGCTTCCGGCTCCCTCGT
DB 1 ATGGGGCTGCTGCGCCCGCTGCGGACGTCCCTCGGGCCGGCTTCCGGCTCCCTCGT 60

QY 61 CGGGGGGGCTCCAGCCCTCCGACAGTACTGTAAGTCAAGTCAAGTCCAGTCCAGTTCCT
DB 61 CGGGGGGGGGCTCCAGCCCTCCGACAGTACTGTAAGTCAAGTCAAGTCCAGTTCCT 120

QY 121 CGAGGAGACCCCGGTGAGAGCTGGGCTCAACGATTACCTAAGACATTGTCTGCCCCAC
DB 121 CGAGGAGACCCCGGTGAGAGCTGGGCTCAACGATTACCTAAGACATTGTCTGCCCCAC 180

QY 181 TAGGAAAGCCCAAGGGCCCGCTGAGAGGGCCCGAGACGTTTGGTTGTAATGAGAGAGTGG
DB 181 TAGGAAAGCCCAAGGGCCCGCTGAGAGGGCCCGAGACGTTTGGTTGTAATGAGAGAGTGG 240

QY 241 CCAAGCTATAGTCTCCAGGCAAGGAGAGGGCCCGCTCAAGCCCTGAGTGTGTCC
DB 241 CCAAGCTATAGTCTCCAGGCAAGGAGAGGGCCCGCTCAAGCCCTGAGTGTGTGTCC 300

QY 301 CTGGCCCTTTGGCCATGTCTCAATTCTCAGAGAAATTCAGGGCTTCAACCTTTTCCCTC
DB 301 CTGGCCCTTTGGCCATGTCTCAATTCTCAGAGAAATTCAGGGCTTCAACCTTTTCCCTC 360

QY 361 GGGCTTGAAGTCTTAACTGAGAGACTTAACTAACTCAACTCGGCCTCCAGAGAGT 420
DB 361 GGGCTTGAAGTCTTAACTGAGAGACTTAACTAACTCAACTCGGCCTCCAGAGAGT 420

QY 421 TCTGGCCAGAGTCTTGAAGGCTCCAGGCTGCTCTGCTGCAAGAGAGAAATCTGAAGTCA
DB 421 TCTGGCCAGAGTCTTGAAGGCTCCAGGCTGCTCTGCTGCAAGAGAGAAATCTGAAGTCA 480

QY 481 GCCCATCTGTTGGAGACCCCTGAGAGAGAGTGGCAATCAAGGCTGAGAGAGGAGAGACT
DB 481 GCCCATCTGTTGGAGACCCCTGAGAGAGAGTGGCAATCAAGGCTGAGAGAGGAGAGACT 540

QY 541 CCGGAGC 546
DB 541 CCGGAGC 546

RESULT 4
ABZ35711 standard; DNA, 606 BP.
ID ABZ35711
XX ABZ35711;
XX 07-FEB-2003 (first entry)

XX Human ephrin A3 encoding polynucleotide SEQ ID NO 19.

XX Double stranded RNA; dsRNA; RNA inhibition; cytostatic; virucide;

XX protosacide; gene expression; antisense; tumour; infection; Plasmodium;

XX Hepatitis C virus; human papilloma virus; gene; ds.

XX Homo sapiens.

XX DE10100588-A1.

XX 18-JUL-2002.

XX 09-JAN-2001; 2001DE-01000588.

XX 09-JAN-2001; 2001DE-01000588.

XX (RIBO-) RIBOPHARMA AG.

XX Kreutzer R, Lämmer S, Rost S, Hadwiger P;

XX WPI; 2002-693450/74.

PT Inhibiting expression of target genes, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.

PS Claim 13; Page 19-20; 100pp; German.

CC The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligonucleotides (dsRNA1 and II), both
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNA1 and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention

XX Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other;

XX Query Match 99.7%; Score 544.4; DB 6; Length 606;

XX Best Local Similarity 99.8%; Pred. No. 5.5e-138;

XX Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGGCTGCTGCGCCCGCTGCGGACGTCCCTCGGGCCGGCTTCCGGCTCCCTCGT
DB 1 ATGGGGCTGCTGCGCCCGCTGCGGACGTCCCTCGGGCCGGCTTCCGGCTCCCTCGT 60

QY 61 CGGGGGGGCTCCAGCCCTCCGACAGTACTGTAAGTCAAGTCAAGTCCAGTTCCT
DB 61 CGGGGGGGGGCTCCAGCCCTCCGACAGTACTGTAAGTCAAGTCAAGTCCAGTTCCT 120

QY 121 CGAGGAGACCCCGGTGAGAGCTGGGCTCAACGATTACCTAAGACATTGTCTGCCCCAC
DB 121 CGAGGAGACCCCGGTGAGAGCTGGGCTCAACGATTACCTAAGACATTGTCTGCCCCAC 180

QY 181 TAGGAAAGCCCAAGGGCCCGCTGAGAGGGCCCGAGACGTTTGGTTGTAATGAGAGTGG
DB 181 TAGGAAAGCCCAAGGGCCCGCTGAGAGGGCCCGAGACGTTTGGTTGTAATGAGAGTGG 240

QY 241 CCAAGCTATAGTCTCCAGGCAAGGAGAGGGCCCGCTCAAGCCCTGAGTGTGTCC
DB 241 CCAAGCTATAGTCTCCAGGCAAGGAGAGGGCCCGCTCAAGCCCTGAGTGTGTGTCC 300

QY 301 CTGGCCCTTTGGCCATGTCTCAATTCTCAGAGAAATTCAGGGCTTCAACCTTTTCCCTC
DB 301 CTGGCCCTTTGGCCATGTCTCAATTCTCAGAGAAATTCAGGGCTTCAACCTTTTCCCTC 360

Db 301 CTGCCCTTGGCCAGTTCATTTCTCAGAGAGATTTCAGCGCTTTCACCCCTTCCCTC 360
 Qy 361 GGCTTTGAGTCTTACCTGAGAGACTTACTACTACTACTCTGGTCCCACTCCAGAGAGT 420
 Db 361 GGCTTTGAGTCTTACCTGAGAGACTTACTACTACTACTCTGGTCCCACTCCAGAGAGT 420
 Qy 421 TCTGCGCAGTCTTGAAGGCTCCAGGCTGTCTGCTGCTGCAAGAGAGAAAGTCTGAGTCA 480
 Db 421 TCTGCGCAGTCTTGAAGGCTCCAGGCTGTCTGCTGCTGCAAGAGAGAAAGTCTGAGTCA 480
 Qy 481 GCCCATCTGTTGGAGCCCTGAGAGAGTGGCAATCAGGGGTGGCCAGAGGGGGGAGCACT 540
 Db 481 GCCCATCTGTTGGAGCCCTGAGAGAGTGGCAATCAGGGGTGGCCAGAGGGGGGAGCACT 540
 Qy 541 CCCAGC 546
 Db 541 CCCAGC 546

RESULT 5
 ID ABL91676 standard; DNA; 606 BP.
 XX ABX09954;
 AC ABX09954;
 DT 23-JAN-2003 (first entry)
 DE Human ephrin A3 DNA fragment SEQ ID 19.
 XX
 KM Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
 XX P1; inhibition; human; ds.
 OS Homo sapiens.
 XX DE10100587-C1.
 PN 21-NOV-2002.
 PD 09-JAN-2001; 2001DE-01000587.
 PF 09-JAN-2001; 2001DE-01000587.
 PR 09-JAN-2001; 2001DE-01000587.
 PA (RIBO-) RIBOPHARMA AG.
 XX
 P1 Kreutzler R, Limmer S, Roest S, Hadwiger P,
 DR WPI; 2002-742209/81.

This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsRNA) that has a double-stranded structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary (ds) to the target gene and the cells are treated with interferon before introduction of dsRNA. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes, developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasmids) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX09956-ABX10075 represent gene fragments used to illustrate the method of the invention

Query Match 99.7%; Score 544.4; DB 6; Length 606;

Best Local Similarity 99.8%; Pred. No. 5.5e-138;
 Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGGGTGTGTCGCCCCCGTGGGAGACTGCTCTTGTGGCCCGGTTCCCTGGCTCCCTG 60
 Db 1 ATGGGGTGTGTCGCCCCCGTGGGAGACTGCTCTTGTGGCCCGGTTCCCTGGCTCCCTG 60
 Qy 61 CGCGGGGGGCTCCAGGCTCCGCGCAGAGTGTACTGAGAACTCCAGTAAACCCAGTGTGCTT 120
 Db 61 CGCGGGGGGCTCCAGGCTCCGCGCAGAGTGTACTGAGAACTCCAGTAAACCCAGTGTGCTT 120
 Qy 121 CGAGGAGAGCCCGTGGTGGAGCTGGGGCTGAAAGATTACTAGACATTGTGCCCCCAG 180
 Db 121 CGAGGAGAGCCCGTGGTGGAGCTGGGGCTGAAAGATTACTAGACATTGTGCCCCCAG 180
 Qy 181 TACGAAAGCCCAAGGGCCCCCTGAGGGCCCGAGAGGTTTGTGTTGTAATGTGGACTGG 240
 Db 181 TACGAAAGCCCAAGGGCCCCCTGAGGGCCCGAGAGGTTTGTGTTGTAATGTGGACTGG 240
 Qy 241 CCAGGCTAATGATGCTGCTGCGCAGAGGAGAGGGCCCCCGGCTTCAAGGCTGGTGTCTCC 300
 Db 241 CCAGGCTAATGATGCTGCTGCGCAGAGGAGAGGGCCCCCGGCTTCAAGGCTGGTGTCTCC 300
 Qy 301 CTGCCCCCTTGGCCATGTTCAATTCTCAGAGAAATTCAGCGCTTCAACCTTTCCTCC 360
 Db 301 CTGCCCCCTTGGCCATGTTCAATTCTCAGAGAAATTCAGCGCTTCAACCTTTCCTCC 360
 Qy 361 GCGTTTGAATCTTAACTGAGAGACTTAACTTCTCAGAGAAATTCAGCGCTTCAACCTTTCCTCC 360
 Db 361 GCGTTTGAATCTTAACTGAGAGACTTAACTTCTCAGAGAAATTCAGCGCTTCAACCTTTCCTCC 360
 Qy 421 TCTGCGCAGTCTTGAAGGCTCCAGGCTGTCTGCTGCTGCAAGAGAGAAAGTCTGAGTCA 480
 Db 421 TCTGCGCAGTCTTGAAGGCTCCAGGCTGTCTGCTGCTGCAAGAGAGAAAGTCTGAGTCA 480
 Qy 481 GCCCATCTGTTGGAGCCCTGAGAGAGTGGCAATCAGGGGTGGCCAGAGGGGGGAGCACT 540
 Db 481 GCCCATCTGTTGGAGCCCTGAGAGAGTGGCAATCAGGGGTGGCCAGAGGGGGGAGCACT 540
 Qy 541 CCCAGC 546
 Db 541 CCCAGC 546

RESULT 6
 ID ABL91676 standard; DNA; 606 BP.
 XX ABL91676;
 AC ABL91676;
 DT 28-MAY-2002 (first entry)
 DE Human polynucleotide SEQ ID NO 19.
 XX
 KM Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
 XX Plasmidum; virus; viroid; cytokine; prion; antisense oligonucleotide;
 XX cytosaratic; virucide; protozoacide; antibacterail; ds.
 OS Homo sapiens.
 XX DE10100586-C1.
 PN 11-APR-2002.
 PD 09-JAN-2001; 2001DE-01000586.
 PF 09-JAN-2001; 2001DE-01000586.
 PR 09-JAN-2001; 2001DE-01000586.
 PA (RIBO-) RIBOPHARMA AG.
 XX
 P1 Kreutzler R, Limmer S, Roest S, Hadwiger P,
 DR WPI; 2002-270454/32.

XX Inhibiting gene expression in cells, useful for e.g. treating tumors, by
 PT introducing double-stranded complementary oligoRNA having unpaired
 PT terminal bases.
 XX

PS Claim 13, Page 20-21; 104pp; German.

CC The invention relates to a method for inhibiting expression of a target
 CC gene (ABL91658-ABL91797) in a cell by introducing at least one
 CC oligoribonucleotide that has a double-stranded structure consisting of at
 CC most 49 sequential nucleotide pairs, with at least part of one strand
 CC complementary with the target gene and has at least one end a single-
 CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
 CC antisense inhibition of gene expression useful e.g. for treating tumors
 CC but the oligoribonucleotides may also be directed against genes present
 CC in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,
 CC animals or plants) or against cytokine, Id, developmental or prion genes.
 CC The method provides more effective inhibition of gene expression than use
 CC of known oligonucleotides, probably because the unpaired
 CC increases stability and thus intracellular concentration

XX
 SQ Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other:

Query Match 99.7%; Score 544.4; DB 6; Length 606;
 Best Local Similarity 99.8%; Pred. No. 5.5e-138;
 Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGGGGGTGCTGCTGCTCCCTGGTGGGAGACTGCTCTGGGCGGGGTTCTTCCCTCCCTCTG	60
DB	1	ATCGGGGTGCTGCTGCTCCCTGGTGGGAGACTGCTCTGGGCGGGGTTCTTCCCTCCCTCTG	60
QY	61	CGGGGGGGCTCCAGSCTCCGSCCACTGACTGAACTCAAGTAACTCCAGGTTGCTT	120
DB	61	CGGGGGGGCTCCAGSCTCCGSCCACTGACTGAACTCAAGTAACTCCAGGTTGCTT	120
QY	121	CGAGGAGACGCGGTGTGTGAGCTGGGCTCAACGATTACATTTGCTGCCCCAC	180
DB	121	CGAGGAGACGCGCGTGTGTGAGCTGGGCTCAACGATTACATTTGCTGCCCCAC	180
QY	181	TACGAAGGCCAGAGGGCCCTGTAGAGGCCCGGAGACGTTTGGTTTACATGTGAGACTGG	240
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QY	241	CCAGGCTATGAGTCTGTCCAGGAGAGGGGCCCGGGCCCTACAAGCGCTGGGTGTGCTCC	300
DB	241	CCAGGCTATGAGTCTGTCCAGGAGAGGGGCCCGGGCCCTACAAGCGCTGGGTGTGCTCC	300
QY	301	CTGCCCTTTGGCCATGTTCAATTTCTCAGAGAAATTCAGCGCTTCAACCTTTCTCCCTC	360
DB	301	CTGCCCTTTGGCCATGTTCAATTTCTCAGAGAAATTCAGCGCTTCAACCTTTCTCCCTC	360
QY	361	GGCTTTGAGTCTTACCTGGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGT	420
DB	361	GGCTTTGAGTCTTACCTGGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGT	420
QY	421	TCTGGCCAGTGTCTTGGGGCTCCAGGTGTCTGTCTGCTGCAAGGAGAGAAAGTCTGAGTCA	480
DB	421	TCTGGCCAGTGTCTTGGGGCTCCAGGTGTCTGTCTGCTGCAAGGAGAGAAAGTCTGAGTCA	480
QY	481	GCCCATCTGTTGGGAGCCCTGGAGAGAGTGGCAATCAGGTTGGCCAGGGGGGAGACT	540
DB	481	GCCCATCTGTTGGGAGCCCTGGAGAGAGTGGCAATCAGGTTGGCCAGGGGGGAGACT	540
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DB	541	CCGAGC 546	

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 Job time : 391.513 sec8

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model1

Run on: April 19, 2005, 09:30:33 ; Search time 118.434 Seconds
(without alignments)
7543.483 Million cell1 updates/sec

Title: US-09-904-954-3_COPY_28_573
Perfect score: 546
Sequence: 1 ATCGGCTGTGCTGCCCTGCT.....GAGGGGGGACACTCCAGC 546

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	546	100.0	636	1	US-08-240-124-3 Sequence 3, Appli
2	546	100.0	636	2	US-08-453-943-3 Sequence 3, Appli
3	546	100.0	636	1	US-09-057-121-3 Sequence 3, Appli
4	546	100.0	636	3	US-09-358-734-3 Sequence 3, Appli
5	544.4	99.7	1182	4	US-09-949-016-1291 Sequence 1291, Ap

ALIGNMENTS

RESULT 1
US-08-240-124-3
; Sequence 3, Application US/08240124
; Patent No. 5516658
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: CERRETTI, DOUGLAS P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; TITLE OF INVENTION: RECEPTOR HEK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESS: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101

QY	DB	Score	Length	ID	Description
QY	1	100.0%	636	1	US-08-240-124-3
DB	28	100.0%	636	2	US-08-453-943-3
QY	61	100.0%	636	1	US-09-057-121-3
DB	88	100.0%	636	3	US-09-358-734-3
QY	121	99.7%	1182	4	US-09-949-016-1291
DB	148	99.7%	1182	4	US-09-949-016-1291
QY	181	99.7%	1182	4	US-09-949-016-1291
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QY	241	99.7%	1182	4	US-09-949-016-1291
DB	268	99.7%	1182	4	US-09-949-016-1291
QY	301	99.7%	1182	4	US-09-949-016-1291

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 7568822
INFORMATION FOR SEQ ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hek-L C6
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 94..630
FEATURE:
NAME/KEY: CDS
LOCATION: 28..633
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 28..93

Query Match 100.0%; Score 546; DB 1; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.9e-142; Indels 0; Gaps 0;
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 361 GGCTTTGAGTCTTACTCGAGAGACTTACTACTACTACTCTCTGGTGGCCCACTCCAGAGAGT 420
Db 388 GGCTTTGAGTCTTACTCGAGAGACTTACTACTACTACTCTCTGGTGGCCCACTCCAGAGAGT 447
Qy 421 TCTGGCCAGTCTTGAAGGCTCCAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 480
Db 448 TCTGGCCAGTCTTGAAGGCTCCAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 507
Qy 481 GCCCATCTGTGGAGAGCCCTGAGAGAGAGTGGCAATCAGGGTGGGGGGGGGAGACT 540
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Qy 541 CCCAGC 546
Db 568 CCCAGC 573

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RESULT 2
US-08-453-943-3
Sequence 3, Application US/08453943
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: IMMUNEX CORPORATION
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO.: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHETICAL: NO

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ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hek-L-C6
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 94..630
NAME/KEY: CDS
LOCATION: 28..633
FEATURE:
NAME/KEY: 619_peptide
LOCATION: 28..93
US-08-453-943-3

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Query Match
Best Local Similarity 100.0%; Score 546; DB 1; Length 636;
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 28 ATGGGGCTGTGGCCCTTGGCCATGTTCAATTTCTAGAGAAATTCCAGCCCTTCAACCTTCTCCCTC 60
Db 61 CGGGGGGGCTTCAAGGCTCCAGCCAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 87
Qy 88 CGGGGGGGCTTCAAGGCTCCAGCCAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 120
Db 121 CGAGAGAGAGCCCGTGTGGAGAGCCCTGAGAGAGAGTGGCAATCAGGGTGGGGGGGGGAGACT 147
Qy 148 CGAGAGAGAGCCCGTGTGGAGAGCCCTGAGAGAGAGTGGCAATCAGGGTGGGGGGGGGAGACT 180
Db 181 TACGAAAGCCCGAGGCCCCCTGAGGGCCCCGAGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 207
Qy 208 TACGAAAGCCCGAGGCCCCCTGAGGGCCCCGAGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 241 CCAGGCTATAGTCTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
Qy 268 CCAGGCTATAGTCTGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 301 CTGGCCCTTGGCCATGTTCAATTTCTAGAGAAATTCCAGCCCTTCAACCTTCTCCCTC 327
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Db 361 GGCTTTGAGTCTTACTCGAGAGACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 387
Qy 388 GGCTTTGAGTCTTACTCGAGAGACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 420
Db 421 TCTGGCCAGTCTTGAAGGCTCCAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 447
Qy 448 TCTGGCCAGTCTTGAAGGCTCCAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 480
Db 481 GCCCATCTGTGGAGAGCCCTGAGAGAGAGTGGCAATCAGGGTGGGGGGGGGAGACT 507
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Db 541 CCCAGC 546
Qy 568 CCCAGC 573

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RESULT 3
US-09-057-121-3
Sequence 3, Application US/09057121
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: IMMUNEX CORPORATION
CITY: SEATTLE

```


TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 AMTI SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: hek-L C6
 FEATURE:

NAME/KEY: mat_peptide
 LOCATION: 94..630
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 28..633
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 28..93

Query Match
 Best Local Similarity 100.0%; Score 546; DB 3; Length 636;
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCGGCTGCTGCCCCCTGCTCGGACTGTCTCTTTGGAGCCGCCCTTCTCGGCTCCCTG
 28 ATCGGCTGCTGCCCCCTGCTCGGACTGTCTCTTTGGAGCCGCCCTTCTCGGCTCCCTG
 61 GCGGGGGCTCCCACTCCCGCACTGTTGAGTCTGTTGAGTCTGTTGAGTCTGTTGAGTCTG
 88 GCGGGGGCTCCCACTCCCGCACTGTTGAGTCTGTTGAGTCTGTTGAGTCTGTTGAGTCTG
 121 GAGAGAGAGCGGTGTGTGAGAGTGTGGCCCTCAACCGATTACCTTACGATTGTTGTTG
 148 GAGAGAGAGCGGTGTGTGAGAGTGTGGCCCTCAACCGATTACCTTACGATTGTTGTTG
 181 TAGAAGAGCCCGAGGCCCTTCAAGGGCCCGAGAGCGTTGTGTTGTTGTTGTTGTTGTTG
 208 TAGAAGAGCCCGAGGCCCTTCAAGGGCCCGAGAGCGTTGTGTTGTTGTTGTTGTTGTTG
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 268 CCAGGCTATGATGTCTCCAGAGAGGCCCCCGAGAGCGTTGTGTTGTTGTTGTTGTTGTTG
 301 CTGCCCTTTGGCCATTGCAATTCTCCAGAAAGATTCAAGGCGTTGTTGTTGTTGTTGTTGTTG
 328 CTGCCCTTTGGCCATTGCAATTCTCCAGAAAGATTCAAGGCGTTGTTGTTGTTGTTGTTGTTG
 361 GGCTTTGAGTCTTACCTTGAAGAGATTCACTTACTACTAATTGAGGCTTTCAACCTTTCTCCCTC
 388 GGCTTTGAGTCTTACCTTGAAGAGATTCACTTACTACTAATTGAGGCTTTCAACCTTTCTCCCTC
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 448 FTGGCCAGTCTTGAAGGCTCCAGGTTGTCTGTCTGCAAGAAGGAGGAAAGTTGAGTCA 480
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 541 CCCAGC 546
 568 CCCAGC 573

RESULT 5
 US-09-949-016-1291
 Sequence 1291, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMOPHISMS IN KNOWN GENES ASSOCIATED
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 1291
 LENGTH: 1182
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-1291

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 Best Local Similarity 99.7%; Score 544.4; DB 4; Length 1182;
 Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 328 CTGCCCTTTGGCCATTGCAATTCTCCAGAAAGATTCAAGGCGTTGTTGTTGTTGTTGTTGTTG
 361 GGCTTTGAGTCTTACCTTGAAGAGATTCACTTACTACTAATTGAGGCTTTCAACCTTTCTCCCTC
 388 GGCTTTGAGTCTTACCTTGAAGAGATTCACTTACTACTAATTGAGGCTTTCAACCTTTCTCCCTC
 421 FTGGCCAGTCTTGAAGGCTCCAGGTTGTCTGTCTGCAAGAAGGAGGAAAGTTGAGTCA 447
 448 FTGGCCAGTCTTGAAGGCTCCAGGTTGTCTGTCTGCAAGAAGGAGGAAAGTTGAGTCA 480
 491 GCCCATCTGTTGGGAGCCCTTGAGAGAGATTCACTCAAGGCTGGGAGGAGAGAGCACT 507
 508 GCCCATCTGTTGGGAGCCCTTGAGAGAGATTCACTCAAGGCTGGGAGGAGAGAGCACT 540
 541 CCCAGC 546
 568 CCCAGC 573

Search completed: April 19, 2005, 22:12:42
 Job time : 118.434 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 09:30:04 ; Search time 2539.69 Seconds
(without alignments)
8183.329 Million cell updates/sec

Title: US-09-904-954-3_COPY_28_573
Perfect score: 546
Sequence: 1 ATCGGGCTGTGCCCTGTCT.....GAGGGGGGACACTCCGAGC 546

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 10.
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing first 1500 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_nc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	544.4	99.7	636	CN289863	170006000
3	544.4	99.7	965	BQ928753	AGENCOURT
4	537	98.4	898	CA454936	AGENCOURT
5	532.4	97.5	707	BB883793	BB883793
6	532.4	97.5	912	BI886252	BI886252
7	521.4	95.5	838	BB890843	BB890843
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9	498.2	91.2	834	CB996846	AGENCOURT
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ALIGNMENTS

RESULT 1
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DEFINITION 17000600263646 GRN_PREHERP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN289865
VERSION CN289865.1 GI:47306279
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 619)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.
TITLE Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 619 Std Error: 0.00.
Location/Qualifiers

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Best Local Similarity 99.8%; Pred. No. 1.3e-129;
Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATCGGGCTGTGCCCTGTCTGCGGACCTGTCTGGCCCGGTTCTCTGCTCCCTCTG	60
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Db	71	CGGGGGGGCTCCAGCTCCGCGACGATGTTACTGGAATCCGATACCCGAGTTGCTT	130
Qy	121	CGAGGAGCGCCGTTGGAGCTGGGGCTCAAGATTACCTAGACATTTCTGGCCGAC	180
Db	131	CGAGGAGCGCCGTTGGAGCTGGGGCTCAAGATTACCTAGACATTTCTGGCCGAC	190
Qy	181	TACGAAAGCCCAAGGGCCCTGAGGGCCCGAGACGTTTGTGATCATGTGAGACTGG	240
Db	191	TACGAAAGCCCAAGGGCCCTGAGGGCCCGAGACGTTTGTGATCATGTGAGACTGG	250
Qy	241	CAAGGCTATGATGCTCTGCGCAGGAGAGGCCCCCGGCTTACAAAGCGCTGGTGTCC	300
Db	251	CAAGGCTATGATGCTCTGCGCAGGAGAGGCCCCCGGCTTACAAAGCGCTGGTGTCC	310
Qy	301	CTGGCCCTTTGGCCATGTTCAATTTCTCAGAGAATTCAGAGGCTTTCCTTCTCCCTC	360
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Qy	361	GGCTTTGAGTTCTTACCTGAGAGACTTACTTACTTACCTGCGTCCCACTCCAGAGAGT	420
Db	371	GGCTTTGAGTTCTTACCTGAGAGACTTACTTACTTACCTGCGTCCCACTCCAGAGAGT	430
Qy	421	TCTGGCCAGTGTGAGAGCTTCAAGGTGTCTGTCTGTGCAAGGAGAAAGTCTGACTCA	480
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Qy	481	GCCATTCCTTTGGAGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	540
Db	491	GCCATTCCTTTGGAGAGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	550
Qy	541	CCGAGC 546	
Db	551	CCGAGC 556	

RESULT 2
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 LOCUS
 DEFINITION 1700060021389 GRN_PREHP Homo sapiens mRNA linear EST 16-MAY-2004
 ACCESSION CN289863
 VERSION CN289863.1 GI:47306277
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi; Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. Brandenberger, R., Wei, H., Zhang, S., Lei, S., Mudge, J., Flisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W. Control human ES cell growth and differentiation using signaling networks that Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA
 TITLE JOURNAL
 COMMENT Contact: Brandenberger R
 Fax: 650 473 8638
 Email: rbrandenberger@geron.com

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /issue_type="embryonic stem cells, DMSO-treated H9 cell line"
 /note="oligo dt primed, full-length enriched cdna library from DMSO-treated h9s cell line H9 (p22) maintained in feeder-free conditions"

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 Query Match
 Best Local Similarity 99.7%; Score 544.4; DB 7; Length 636;
 Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGGGCTGTCGCCCTGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 60
 43 ATCGGCTCTGTCGCCCTGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 60
 61 CGGGGGCTCTGTCGCCCTGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 102
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 121 CGAGGAGACGGCGGTGGAGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 120
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 181 TAGGAAGGCGCGGGTGGAGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 180
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 403 GGCTTTGAGTTTAACTTGAAGAGACTTACTACTACTACTACTACTACTACTACTACTACTACT 402
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ORIGIN
 Query Match
 Best Local Similarity 99.8%; Score 544.4; DB 5; Length 965;
 Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGGGCTGTCGCCCTGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 60
 56 ATGGGGCTGTCGCCCTGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 60
 61 CGGGGGCTCTGTCGCCCTGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 115
 116 CGGGGGCTCTGTCGCCCTGCTGGAGACGTCTCTGGGGCGGGTTCCTGCTCCCTCCCTCG 115
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 /clone_id="NIH_MGC_40"
 /note="Organ: prostate; Vector: pORF7; Site: 1; XhoI; directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene, Berkeley) using ZAP-cDNA synthesis kit Note: this is a NIH_MGC Library."

RESULT 3
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 LOCUS
 DEFINITION BQ928753 965 bp mRNA linear EST 20-AUG-2002
 AGENCOURT_10036172 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6481391
 ACCESSION BQ928753
 VERSION BQ928753.1 GI:22343784
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominoidea; Homo. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: gadsb-remail.nih.gov
 Tissue Procurement: DCTD/DP
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LINL
 http://image.lnl.gov
 Plate: LINC2662 row: k column: 24
 High quality sequence stop: 635.
 Location/Qualifiers
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Db 176 CGAGGAGACCGCCGTGTGAGACTGGGCTCAACGATTACTAGACATTTGCTGCCCCC 235
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 181 TACGAAGGCCAGAGCCCGCCCTGAGGGCCCGGAGACGTTTGTGTAATGATGGACTGG 240
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 Db 236 TACGAAGGCCAGAGCCCGCCCTGAGGGCCCGGAGACGTTTGTGTAATGATGGACTGG 235
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 QY 241 CCAAGGCTATGAGTCTGCGCAGGAGAGGGCCCGCCCTTCAAGCCCTGGGTGTCTCC 300
 296 CCAAGGCTATGAGTCTGCGCAGGAGAGGGCCCGCCCTTCAAGCCCTGGGTGTCTCC 355
 |||||
 QY 301 CTGCGCTTTGGCCATGTTCAATTTCTCAGAGAAATTGAGCGCTTACAGCTTTCTCCCTC 360
 356 CTGCGCTTTGGCCATGTTCAATTTCTCAGAGAAATTGAGCGCTTACAGCTTTCTCCCTC 415
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 Db 361 GGGTTTGAAGTTCTTACTCTGAGAGACTTACTACTACTCTGGGTCCTCCAGAGAGT 420
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 QY 416 GGGTTTGAAGTTCTTACTCTGAGAGACTTACTACTACTCTGGGTCCTCCAGAGAGT 475
 |||||
 Db 421 TCTGGCCAGTCTTGGAGGCTCCAGGTTCTGTCTGTGCAAGGAGAAAGTCTGAGTCA 480
 476 TCTGGCCAGTCTTGGAGGCTCCAGGTTCTGTCTGTGCAAGGAGAAAGTCTGAGTCA 535
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 QY 481 GCCCATCTCTTGGAGGAGCCCTGGAGAGAGTGGCAATCAGGGTGGCGAGGGGGAGACT 540
 536 GCCCATCTCTTGGAGGAGCCCTGGAGAGAGTGGCAATCAGGGTGGCGAGGGGGAGACT 595
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 QY 541 CCCAGC 546
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 Db 596 CCCAGC 601

RESULT 4
 CA454936 898 bp mRNA linear EST 12-NOV-2002
 LOCUS AGENCOURT_10714679 MABPCL Homo sapiens cDNA clone IMAGE:6722424 5',
 DEFINITION mRNA sequence.
 ACCESSION CA454936
 VERSION CA454936.1 GI:24905152
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 898)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabrs-r@mail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Ira Paetan
 cDNA Library Preparation: Invitrogen Corp
 DNA Sequencing by: Agencourt Bioscience Corporation
 DNA distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM14285 row: b column: 24
 High quality sequence stop: 473.
 Location/Qualifiers
 1. 898
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6722424"
 /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
 HERF-HME1, LNCAP"
 /lab_host="EMDH10B"
 /clone_lib="MABPCL"
 /note="Vector: PCMV-SPORE; Site_1: EcorV; Site_2: Not I;
 Subcloned with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dr. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,

FEATURES
 source

ORIGIN
 Bungkook Lee & Ira Paetan: Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."
 Query Match 98.4%; Score 537; DB 6; Length 898;
 Best Local Similarity 98.9%; Pred. No. 1.1e-127;
 Matches 540; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 ATGGGGTGTGTCGCGCCCTGCGAGACTGTCCTCTGGGGCCGCTTCCCTGCTCCCTCTG 60
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 56 ATGCGGGTGTGTCGCGCCCTGCGAGACTGTCCTCTGGGGCCGCTTCCCTGCTCCCTG 115
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 QY 61 CGCGGGGGCTCCAGCCTCCGACGTAAGTCTGAACTCCAGTAAACCCAGAGTTGCTT 120
 116 CGCGGGGGCTCCAGCCTCCGACGTAAGTCTGAACTCCAGTAAACCCAGAGTTGCTT 175
 |||||
 QY 121 CGAGAGACGCGGTGTGAGACTGGGCTTCAAGAAATTACTAGACATTTGTCTGCCCCAC 180
 176 CGAGAGACGCGGTGTGAGACTGGGCTTCAAGAAATTACTAGACATTTGTCTGCCCCAC 235
 |||||
 Db 181 TACGAAGGCCAGAGCCCGCCCTGAGGGCCCGGAGACGTTTGTGTAATGATGGACTGG 240
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 QY 236 TACGAAGGCCAGAGCCCGCCCTGAGGGCCCGGAGACGTTTGTGTAATGATGGACTGG 295
 |||||
 Db 241 CCAAGGCTATGAGTCTGCGCAGGAGAGGGCCCGCCCTTCAAGCCCTGGGTGTCTCC 300
 296 CCAAGGCTATGAGTCTGCGCAGGAGAGGGCCCGCCCTTCAAGCCCTGGGTGTCTCC 355
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 QY 301 CTGCGCTTTGGCCATGTTCAATTTCTCAGAGAAATTGAGCGCTTACAGCTTTCTCCCTC 360
 356 CTGCGCTTTGGCCATGTTCAATTTCTCAGAGAAATTGAGCGCTTACAGCTTTCTCCCTC 415
 |||||
 Db 361 GGGTTTGAAGTTCTTACTCTGAGAGACTTACTACTACTCTGGGTCCTCCAGAGAGT 420
 416 GGGTTTGAAGTTCTTACTCTGAGAGACTTACTACTACTCTGGGTCCTCCAGAGAGT 475
 |||||
 QY 421 TCTGGCCAGTCTTGGAGGCTCCAGGTTCTGTCTGTGCAAGGAGAAAGTCTGAGTCA 480
 476 TCTGGCCAGTCTTGGAGGCTCCAGGTTCTGTCTGTGCAAGGAGAAAGTCTGAGTCA 535
 |||||
 Db 481 GCCCATCTCTTGGAGGAGCCCTGGAGAGAGTGGCAATCAGGGTGGCGAGGGGGAGACT 540
 536 GCCCATCTCTTGGAGGAGCCCTGGAGAGAGTGGCAATCAGGGTGGCGAGGGGGAGACT 595
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 QY 541 CCCAGC 546
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 Db 596 TCCAGC 601

RESULT 5
 BE883793 707 bp mRNA linear EST 20-OCT-2000
 LOCUS 601506189F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907510 5',
 DEFINITION mRNA sequence.
 ACCESSION BE883793
 VERSION BE883793.1 GI:10332569
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 707)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabrs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: L1AM9718 row: b column: 23
High quality sequence stop: 706.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="RNA"
/dx_xref="taxon:9606"
/clone="IMAGE:3907510"
/journal="
/issue_type="1:siomycosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NciI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo df.
Average insert size 2.1 kb."

ORIGIN

Query Match 97.5%; Score 532.4; DB 2; Length 707;
Best Local Similarity 99.6%; Pred. No. 1.7e-126;
Matches 544; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

1 ATGCGGCTGCTGCCCCGCTGGAGACTGTCTGCGGGCCGGGTTCCGGCTCCCTCTG
49 ATGCGGCTGCTGCCCCGCTGGAGACTGTCTGCGGGCCGGGTTCCGGCTCCCTCTG
61 CGCGGGGGCTCCAGGCTCCCGCAGCTAGTCTAGTGAACCCAGGTTGCTT
109 CGGGGGGGCTCCAGGCTCCCGCAGCTAGTCTAGTGAACCCAGGTTGCTT
121 CGAGGAGAGCGGCTGTGAGAGCTGGGCTTAAAGATTAAGTGAACATTTGCTG
169 CGAGGAGAGCGGCTGTGAGAGCTGGGCTTAAAGATTAAGTGAACATTTGCTG
181 TAGGAAGGCCGAGGGCCCGCTGAGGGCCCGGAGAGCTTTGTATGATGTGGACTGG
229 TAGGAAGGCCGAGGGCCCGCTGAGGGCCCGGAGAGCTTTGTATGATGTGGACTGG
241 CGAGGCTATGATGCTCCAGGAGCAAGAGGCCCCCGGGCCCTAACAGGCTGGTGTCC
288 CGAGGCTATGATGCTCCAGGAGCAAGAGGCCCCCGGGCCCTAACAGGCTGGTGTCC
301 CTGCCCCCTTGGCCAGTTCATATCTCAGAGAAATTCAGGCTTCAACCTTTCTCC
348 CTGCCCCCTTGGCCAGTTCATATCTCAGAGAAATTCAGGCTTCAACCTTTCTCC
361 GGCTTTGAGTTCCTTACCTGAGAGACTTACTACTACTACTACTACTACTACTACT
408 GGCTTTGAGTTCCTTACCTGAGAGACTTACTACTACTACTACTACTACTACTACT
421 TCTGGCCAGTGTCTGAGGGCTCCAGGCTGTCTGCTGCAAGAGAGAAATCTGAGTCA
468 TCTGGCCAGTGTCTGAGGGCTCCAGGCTGTCTGCTGCAAGAGAGAAATCTGAGTCA
481 GCCCATCTGTTGGAGGCTCCCTGAGAGAGTGGCAATCAAGGGTGGCGGAGAGCACT
528 GCCCATCTGTTGGAGGCTCCCTGAGAGAGTGGCAATCAAGGGTGGCGGAGAGCACT
541 CCCAGC 546
588 CCCAGC 593

RESULT 6
BI868252
LOCUS BI868252
DEFINITION 603392205F1_NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402208 5,
ACCESSION BI868252
VERSION BI868252.1 GI:16041925
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 912)
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rs9abds-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: L1AM2025 row: j column: 01
High quality sequence stop: 806.
Location/Qualifiers
1..912
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/mol_type="RNA"
/dx_xref="taxon:9606"
/clone="IMAGE:5402208"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NciI; Site 2: Sall; Cloned unidirectionally; oligo-df primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN

Query Match 97.5%; Score 532.4; DB 4; Length 912;
Best Local Similarity 99.6%; Pred. No. 1.7e-126;
Matches 544; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

1 ATGCGGCTGCTGCCCCGCTGGAGACTGTCTGCGGGCCGGGTTCCGGCTCCCTCTG
39 ATGCGGCTGCTGCCCCGCTGGAGACTGTCTGCGGGCCGGGTTCCGGCTCCCTCTG
61 CGCGGGGGCTCCAGGCTCCCGCAGCTAGTCTAGTGAACCCAGGTTGCTT
99 CGGGGGGGCTCCAGGCTCCCGCAGCTAGTCTAGTGAACCCAGGTTGCTT
121 CGAGGAGAGCGGCTGTGAGAGCTGGGCTTAAAGATTAAGTGAACATTTGCTG
159 CGAGGAGAGCGGCTGTGAGAGCTGGGCTTAAAGATTAAGTGAACATTTGCTG
181 TAGGAAGGCCGAGGGCCCGCTGAGGGCCCGGAGAGCTTTGTATGATGTGGACTGG
219 TAGGAAGGCCGAGGGCCCGCTGAGGGCCCGGAGAGCTTTGTATGATGTGGACTGG
241 CGAGGCTATGATGCTCCAGGAGCAAGAGGCCCCCGGGCCCTAACAGGCTGGTGTCC
278 CGAGGCTATGATGCTCCAGGAGCAAGAGGCCCCCGGGCCCTAACAGGCTGGTGTCC
301 CTGCCCCCTTGGCCAGTTCATATCTCAGAGAAATTCAGGCTTCAACCTTTCTCC
338 CTGCCCCCTTGGCCAGTTCATATCTCAGAGAAATTCAGGCTTCAACCTTTCTCC
361 GGCTTTGAGTTCCTTACCTGAGAGACTTACTACTACTACTACTACTACTACTACT
398 GGCTTTGAGTTCCTTACCTGAGAGACTTACTACTACTACTACTACTACTACTACT
421 TCTGGCCAGTGTCTGAGGGCTCCAGGCTGTCTGCTGCAAGAGAGAAATCTGAGTCA
457 TCTGGCCAGTGTCTGAGGGCTCCAGGCTGTCTGCTGCAAGAGAGAAATCTGAGTCA
480 TCTGGCCAGTGTCTGAGGGCTCCAGGCTGTCTGCTGCAAGAGAGAAATCTGAGTCA
517 GCCCATCTGTTGGAGGCTCCCTGAGAGAGTGGCAATCAAGGGTGGCGGAGAGCACT
540 GCCCATCTGTTGGAGGCTCCCTGAGAGAGTGGCAATCAAGGGTGGCGGAGAGCACT
577

RESULT 6
BI868252
LOCUS BI868252
DEFINITION 603392205F1_NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402208 5,
ACCESSION BI868252
VERSION BI868252.1 GI:16041925
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

QY 541 CCCAGC 546
Db 578 CCCAGC 583

RESULT 7
BE890843 838 bp mRNA linear EST 20-OCT-2000
LOCUS 601431292F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916487 5',
DEFINITION mRNA sequence.
ACCESSION BE890843
VERSION BE890843.1 GI:10349570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: sgabds-rc@mail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)
DNA Sequencing by: Inqyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLML at:
http://image.lnl.gov
Plate: HAM9741 row: h column: 24
High quality sequence stop: 707.
Location/Qualifiers

FEATURES

source
1..838
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3916487"
/issue_type="melanotic melanoma"
/lab_host="DHI08 (phage-resistant)"
/clone_id="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 95.5%; Score 521.4; DB 2; Length 838;

Best Local Similarity 99.5%; Pred. No. 1.2e-123;

Matches 544; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 ATGGGCTGTGCTCCCTGCTGGCGGACTGCTCTCTCCCTCCCTCCCTG 60
Db 71 ATGGGCTGTGCTCCCTGCTGGCGGACTGCTCTCTCCCTCCCTCCCTG 130
QY 61 CGGGGGGGCTCCAGCTCCCGCAGTGTACTGTGAACTCGAATACCCAGGTTGCTT 120
Db 131 CGGGGGGGCTCCAGCTCCCGCAGTGTACTGTGAACTCGAATACCCAGGTTGCTT 190
QY 121 CGAGGAGACCGCGGTGTGAGAGTGGGCTCAAGATTACTAGACATTGCTGCCCCGAC 180
Db 191 CGAGGAGACCGCGGTGTGAGAGTGGGCTCAAGATTACTAGACATTGCTGCCCCGAC 250
QY 181 TAGGAGAGCCCGAGGCGCCCTGAGAGGCGCCCGAGAGCGTTTGTGTCATGAGTGG 240
Db 251 TAGGAGAGCCCGAGGCGCCCTGAGAGGCGCCCGAGAGCGTTTGTGTCATGAGTGG 309
QY 241 CCAAGGCTATGATGCTGTGAGGAGGAGGCGCCCGGCGCTCAAGCGCTGGGAGTGGTCC 300
Db 310 CCAAGGCTATGATGCTGTGAGGAGGAGGCGCCCGGCGCTCAAGCGCTGGGAGTGGTCC 369
QY 301 CTGGCCCTTTGGCCATGTTCAATTCTCAGAGAAATTAAGCGCTTCAAGCCTTTCTCCCTC 360

Db 370 CTGGCCCTTTGGCCATGTTCAATTCTCAGAGAAATTAAGCGCTTCAAGCCTTTCTCCCTC 429
QY 361 GGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACTCTGGGCGCCACTCCAGAGAGT 420
Db 430 GGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACTCTGGGCGCCACTCCAGAGAGT 489
QY 421 TCTGGCCAGGCTGTGAGAGCTCCAGGTGTCTGTCTGTCTGCAAGAGAGAAATGCTGACTCA 480
Db 490 TCTGGCCAGGCTGTGAGAGCTCCAGGTGTCTGTCTGTCTGCAAGAGAGAAATGCTGACTCA 549
QY 481 GCCCATCTCTGTGGAGAGCCCTGAGAGAGTGGGCAATCAGGGTGGCGA-GGGGGGAGAC 539
Db 550 GCCCATCTCTGTGGAGAGCCCTGAGAGAGTGGGCAATCAGGGTGGCGAAGCGGGGGAGAC 609
QY 540 TCCCAGC 546
Db 610 TCCCAGC 616

RESULT 8
CN289864
LOCUS CN289864 663 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424723908 GRN ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN289864
VERSION CN289864.1 GI:47306278
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Brandenberger R., Wei H., Zhang S., Lei S., Murage J., Fisk G., J.,
Li Y., Xu C., Fang R., Quegler K., Rao M.S., Mandalam R.,
Lebkowski J and Stanton L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Genor Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8558
Fax: 650 473 7760
Email: rbrandenberger@genor.com
Insert Length: 663 Std Error: 0.00.
Location/Qualifiers

FEATURES

source
1..663
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_id="GRN ES"
/note="Oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 91.5%; Score 499.4; DB 7; Length 663;

Best Local Similarity 99.8%; Pred. No. 5.3e-118;

Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 CTGGGCTCCCTCTGTGGCGGGGCTCCAGCTCCGCGAGTACTGAGAACTCGAGT 105
Db 12 CTGGGCTCCCTCTGTGGCGGGGCTCCAGCTCCGCGAGTACTGAGAACTCGAGT 71
QY 106 AACCCAGGTTGCTTGGAGAGAGCGCGTGTGAGAGTGGGCGCTCAACGATTAAGTAC 165
Db 72 AACCCAGGTTGCTTGGAGAGAGCGCGTGTGAGAGTGGGCGCTCAACGATTAAGTAC 131
QY 166 ATTGTCTGCCCCCACTAAGAGGCGCCCGCTGAGGGCCCGAGAGCGTTTGTCTTTG 225
Db 132 ATTGTCTGCCCCCACTAAGAGGCGCCCGCTGAGGGCCCGAGAGCGTTTGTCTTTG 191

QY 226 TACATGGTGGACTGGCCAGGCTATGATGCTTCCAGGACAGAGGCCCTCCGAGCTTACAAG
 Db 192 TACATGGTGGACTGGCCAGGCTATGATGCTTCCAGGACAGAGGCCCTCCGAGCTTACAAG
 QY 286 CGCTGGGTGTGGCTCCCTCCCTCTTTGGCCATGTTCAATTTCTGAGAGAAATTCACGGCTTG
 Db 252 CGCTGGGTGTGGCTCCCTCCCTCTTTGGCCATGTTCAATTTCTGAGAGAAATTCACGGCTTG
 QY 346 AACACCTTTCTCCCTGGCTTGGAGTTCTTACTGGAGAGACTTACTTACTTACTTCTGCTG
 Db 312 AACACCTTTCTCCCTGGCTTGGAGTTCTTACTGGAGAGACTTACTTACTTACTTCTGCTG
 QY 406 CCACTCTCAGAGAGTTCTGGCCAGAGCTTGGAGGCTCCAGAGTGTCTGCTGCTGCAAGAG
 Db 372 CCACTCTCAGAGAGTTCTGGCCAGAGCTTGGAGGCTCCAGAGTGTCTGCTGCTGCAAGAG
 QY 466 AGGAAGTCTGAGTCCAGCCCAATCTCTTGGAGGCTCCAGAGTGTCTGCTGCTGCAAGAG
 Db 432 AGGAAGTCTGAGTCCAGCCCAATCTCTTGGAGGCTCCAGAGTGTCTGCTGCTGCAAGAG
 QY 526 CGAGGGGGGAGCACTCCCGAC 546
 Db 492 CGAGGGGGGAGCACTCCCGAC 512

RESULT 9
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 LOCUS
 DEFINITION AGNCOURT_1366148 NIH_MGC_148 Homo sapiens linear EST 01-MAY-2003
 ACCESSION IMAGE:30332601.5, mRNA sequence.
 VERSION CB996846
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC Http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 DNAs sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information
 http://image.llnl.gov
 Plate: NDM349 row: 0 column: 10
 High quality sequence stop: 514.
 Location/Qualifiers
 1. 834

FEATURES
 source
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 /clone="IMAGE:30332601"
 /tissue_type="pre-clamptic placenta"
 /lab_host="DH10B_Tonak"
 /clone_id="NIH_MGC_148"
 /note="Organ: Placenta; Vector: pBluescript; Site: 1;
 all-1XhoI; Site: 2; BamHI; Library is oligo-dT primed and
 directionally cloned using primer:
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
 library enriched for full-length clones and constructed
 using the Cap-trapper method (Carninci, in preparation).
 Library constructed by M. Brownstein (NHGRI/MHGRRI,
 National Institutes of Health). Note: this is a NIH_MGC
 Library."

mol_type="mRNA"
 taxon="9606"
 IMAGE:30332601
 pre-clamptic placenta
 DH10B_Tonak
 NIH_MGC_148
 Organ: Placenta; Vector: pBluescript; Site: 1; all-1XhoI; Site: 2; BamHI; Library is oligo-dT primed and directionally cloned using primer: 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/MHGRRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 91.2%; Score 498.2; DB 6; Length 834;
 Best Local Similarity 97.2%; Pred. No. 1,16-117;
 Matches 528; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
 1 AAGGAGGCTGGTGGCCCTCTGCTGGAGACTGTCTCTGGCCCGCTTCTCGCTGGCTTCCCTCTG
 99 ATGAGAGCTGCTGCCCTGCTGGACTGTCTCTGGCCCGCTTCTCGCTGGCTTCCCTCTG
 61 CGGGGGGGCTCCAGGCTCCCGCCAGAGTGTACTGGAATCCAGTAATCCAGAGTTCCTT
 159 CGGGGGGGCTCCAGGCTCCCGCCAGAGTGTACTGGAATCCAGTAATCCAGAGTTCCTT
 121 CGAGGAGAGCCGCTGGTGGAGTGGGCTCAACGATTAAGTAACATTTGCTGCCCGCCAG
 219 CGAGGAGAGCCGCTGGTGGAGTGGGCTCAACGATTAAGTAACATTTGCTGCCCGCCAG
 181 TAGGAGGCTCCAGAGGCTCCGCTGAGAGAGGAGAGGCTTGTGTAATGTTGACTG
 279 TACGAGGCTCCAGAGGCTCCGCTGAGAGAGGAGAGGCTTGTGTAATGTTGACTG
 241 CAGGCTATGAGTCTGTGCGAGGAGAGAGGAGAGGCTTGTGTAATGTTGACTG
 339 CAGGCTATGAGTCTGTGCGAGGAGAGAGGAGAGGCTTGTGTAATGTTGACTG
 301 CTGGCCCTTGGCCAGAGTCAATTTCTGAGAGAGATTCAGAGGCTTGTGTAATGTTGACTG
 399 CTGGCCCTTGGCCAGAGTCAATTTCTGAGAGAGATTCAGAGGCTTGTGTAATGTTGACTG
 361 GGCCTTGTGAGTCTTACTGCTGAGAGAGACTTACTTACTTACTTACTTACTTACTTACTT
 459 GCTTTTGTGAGTCTTACTGCTGAGAGAGACTTACTTACTTACTTACTTACTTACTTACTT
 421 TGTGGCCAGTGTCTTGGGCTCCAGAGTGTCTGCTGCT -GAAAGAGAGAGAGTGTGATG
 519 TGTGGCCAGTGTCTTGGGCTCCAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
 480 AGCCCAATCTTGTGGAGAGCCTT -GAGAGAGTGGCAATTCAGAGGCTGGAGGGGGAGGA
 579 ATCCCATCTGTTGGAGAGCCTTGGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG
 539 CTC 541
 Db 639 CAC 641

RESULT 10
 LOCUS CD671399
 DEFINITION f904c02.y1 Human Iris cDNA (Normalized): fg Homo sapiens CDNA clone
 ACCESSION CD671399
 VERSION CD671399.1 GI:32173139
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC Http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 DNAs sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information
 http://image.llnl.gov
 Plate: NDM349 row: 0 column: 10
 High quality sequence stop: 514.
 Location/Qualifiers
 1. 592

mol_type="mRNA"
 taxon="9606"
 IMAGE:30332601
 pre-clamptic placenta
 DH10B_Tonak
 NIH_MGC_148
 Organ: Placenta; Vector: pBluescript; Site: 1; all-1XhoI; Site: 2; BamHI; Library is oligo-dT primed and directionally cloned using primer: 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/MHGRRI, National Institutes of Health). Note: this is a NIH_MGC Library."

JOURNAL MEDLINE PUBLISHED COMMENT
 Section on Molecular Structure and Function
 National Eye Institute
 6/3/31, NIH, Bethesda, MD 20892-2740, USA
 Tel.: 301 402 3452

Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 04 row: c column: 02
 Seq primer: M13RPI reverse primer (ABI)
 Location/Qualifiers
 1..592

Source
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="fg04c02"
 /issue_type="Iris"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="Human Iris cDNA (Normalized): fg"
 /note="Organ: Eye; Vector: pCMVSPORT6; A human iris library (Irx) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 91.1%; Score 497.4; DB 6; Length 592;
 Best Local Similarity 99.8%; Pred. No. 1.7e-117;
 Matches 498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGGCTGTGCCCCCTGCTGCGGACTGCTCTGCGGCCGGCTTCTCGGCTCCCTCTG 60
 DB ATGGGGCTGTGCCCCCTGCTGCGGACTGCTCTGCGGCCGGCTTCTCGGCTCCCTCTG 153
 QY 61 CGGGGGGGCTTCCAGCTCCCGCAGTGTACTGTGAACTCCAGTAACTCCGAGGTGCTT 120
 DB CGGGGGGGCTTCCAGCTCCCGCAGTGTACTGTGAACTCCAGTAACTCCGAGGTGCTT 213
 QY 121 CGAGGAGACGCGGTGTGAGCTGAGCTGAGGCTCAAGATTACTAGACATTGCTGCCCCAC 180
 DB CGAGGAGACGCGGTGTGAGCTGAGCTGAGGCTCAAGATTACTAGACATTGCTGCCCCAC 273
 QY 181 TACGAAAGCCAGGAGCCCTTGAAGGCCCCGAGACGTTTGCTTTGTAACATGATGACTGG 240
 DB TACGAAAGCCAGGAGCCCTTGAAGGCCCCGAGACGTTTGCTTTGTAACATGATGACTGG 333
 QY 241 CCAGGCTATGATGCTCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 DB CCAGGCTATGATGCTCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 393
 QY 301 CTGCCCCCTTGGCCATGTTCAATTCTCAGAGAAGATTGAGGGCTTCAACCTTTTCCCTC 360
 DB CTGCCCCCTTGGCCATGTTCAATTCTCAGAGAAGATTGAGGGCTTCAACCTTTTCCCTC 453
 QY 361 GGCTTTGAGTTCCTTACCTGAGAGACTTACTACTACATCTGAGTCCCACTCCAGAGAGT 420
 DB GGCTTTGAGTTCCTTACCTGAGAGACTTACTACTACATCTGAGTCCCACTCCAGAGAGT 513
 QY 421 TCTGGCCAGTGTCTTGAAGGCTCCAGGCTGCTGTGCTGCAAGAGAGAAAGTCTGAGTCA 480
 DB TCTGGCCAGTGTCTTGAAGGCTCCAGGCTGCTGTGCTGCAAGAGAGAAAGTCTGAGTCA 573
 QY 481 GCCCATCCTGTTGGAGCC 499
 DB GCCCATCCTGTTGGAGCC 592

Search completed: April 19, 2005, 21:57:12
 Job time : 2540.83 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 23:10:12 ; Search time 35.3289 Seconds
(without alignments)
1684.011 Million cell updates/sec

Title: US-09-904-954-4_COPY_1_179
Perfect score: 989
Sequence: 1 MRLILPLRLRYLMAAFLGSPPL.....SAHPVSGSPGSGTSGMRGCD 179

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1421835 seqs, 332370683 residues
Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing first 1500 summaries

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- 1: Published Applications AA:*
 - 2: /cgn2_6/prodmeta/2/pubppaa/US07_PUBSCOMB.pep:*
 - 3: /cgn2_6/prodmeta/2/pubppaa/PCT_NEW_PUB.pep:*
 - 4: /cgn2_6/prodmeta/2/pubppaa/US06_PUBSCOMB.pep:*
 - 5: /cgn2_6/prodmeta/2/pubppaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/prodmeta/2/pubppaa/PCTUS_PUBSCOMB.pep:*
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 - 11: /cgn2_6/prodmeta/2/pubppaa/US09C_PUBSCOMB.pep:*
 - 12: /cgn2_6/prodmeta/2/pubppaa/US09_NEW_PUB.pep:*
 - 13: /cgn2_6/prodmeta/2/pubppaa/US10A_PUBSCOMB.pep:*
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 - 18: /cgn2_6/prodmeta/2/pubppaa/US11_NEW_PUB.pep:*
 - 19: /cgn2_6/prodmeta/2/pubppaa/US60_NEW_PUB.pep:*
 - 20: /cgn2_6/prodmeta/2/pubppaa/US60_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	989	100.0	201	9 US-09-904-954-4	Sequence 4, Appli
2	989	100.0	201	17 US-10-698-907-12	Sequence 12, Appli
3	971	98.2	201	13 US-10-138-787-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-904-954-4
; Sequence 4, Application US/09904954
; Patent No. US20020010325A1
; GENERAL INFORMATION:

APPLICANT: BECKMANN, M. P.
 CERRETTI, DOUGLAS P.
 TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE RECEPTOR HEK
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMUNEX CORPORATION
 STREET: 51 UNIVERSITY STREET
 CITY: SEATTLE
 STATE: WASHINGTON
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple System 7.1
 SOFTWARE: Microsoft Word for Apple, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/904,954
 FILING DATE: 12-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/240,124
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/114,426
 FILING DATE: 30-AUG-1993
 APPLICATION NUMBER: US 08/109,745
 FILING DATE: 20-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: SEESH, KATHRYN A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2814-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELELEX: 756822
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 201 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-904-954-4
 Query Match 100.0%; Score 989; DB 9; Length 201;
 Best Local Similarity 100.0%; Pred. No. 2.4e-96;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	121	GFEFLPGEFTYYYSIVPPSSGQCLRLQVSVCKERRKESBAHPVGSFGESGTSGMRCGD	179
QY	1	MRLILPLRLRYLMAAFLGSPPLRGGSSLRHYVYMNNSNRLLRGDAVVELGINDYDIYCPH	60
DB	1	MRLILPLRLRYLMAAFLGSPPLRGGSSLRHYVYMNNSNRLLRGDAVVELGINDYDIYCPH	60
QY	61	YEGPPEPEGETFALVYWDMPGYESSCOAEGPRAYKRWVCSLPGHVQFSEKIQRTFPTFSL	120
DB	61	YEGPPEPEGETFALVYWDMPGYESSCOAEGPRAYKRWVCSLPGHVQFSEKIQRTFPTFSL	120
QY	121	GFEFLPGEFTYYYSIVPPSSGQCLRLQVSVCKERRKESBAHPVGSFGESGTSGMRCGD	179
DB	121	GFEFLPGEFTYYYSIVPPSSGQCLRLQVSVCKERRKESBAHPVGSFGESGTSGMRCGD	179

RESULT 2
 US-10-698-907-12
 ; Sequence 12, Application US/10698907
 ; Publication No. US20050049194A1
 ; GENERAL INFORMATION:
 APPLICANT: Pilsen, Jonas
 APPLICANT: Holmberg, Johan
 TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
 ; TITLE OF INVENTION: Proliferation
 ; FILE REFERENCE: 21882-529 UTIL
 ; CURRENT APPLICATION NUMBER: US/10/698,907

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CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: US 60/460,488
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 10/291,290
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/393,272
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/345,206
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
US-10-698-907-12

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Query Match
Best Local Similarity 100.0%; Score 989; DB 17; Length 201;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRLLPLRLTYVMAAFLGSPPLRGSSSLRHHVYWNNSNPRLLRGDVAVVEIGLNDYLDIVCPH 60
DB 1 MRLLPLRLTYVMAAFLGSPPLRGSSSLRHHVYWNNSNPRLLRGDVAVVEIGLNDYLDIVCPH 60
QY 61 YEGPDPPEGPEPTFALYVMDWPGYESSCAEGPRAYRWVCSLPEFGHVQFSEKIQRFPTPSSL 120
DB 61 YEGPDPPEGPEPTFALYVMDWPGYESSCAEGPRAYRWVCSLPEFGHVQFSEKIQRFPTPSSL 120
QY 121 GFEPFLPGETYYTYSVPTPESSGQCRLQVSVCCCKERKSESNAHPVGSFGSGTSGWRGCD 179
DB 121 GFEPFLPGETYYTYSVPTPESSGQCRLQVSVCCCKERKSESNAHPVGSFGSGTSGWRGCD 179

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RESULT 3
US-10-138-787-8
Sequence 8, Application US/10138787
Publication No. US20020172984A1
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/10/138,787
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/214,631
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: PCT/CA97/00473
PRIOR FILING DATE: 1997-07-04
PRIOR APPLICATION NUMBER: 60/021,272
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
US-10-138-787-8

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Query Match
Best Local Similarity 98.2%; Score 971; DB 13; Length 201;
Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MRLLPLRLTYVMAAFLGSPPLRGSSSLRHHVYWNNSNPRLLRGDVAVVEIGLNDYLDIVCPH 60
DB 1 MRLLPLRLTYVMAAFLGSPPLRGSSSLRHHVYWNNSNPRLLRGDVAVVEIGLNDYLDIVCPH 60
QY 61 YEGPDPPEGPEPTFALYVMDWPGYESSCAEGPRAYRWVCSLPEFGHVQFSEKIQRFPTPSSL 120
DB 61 YEGPDPPEGPEPTFALYVMDWPGYESSCAEGPRAYRWVCSLPEFGHVQFSEKIQRFPTPSSL 120

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QY 121 GFEPFLPGETYYTYSVPTPESSGQCRLQVSVCCCKERKSESNAHPVGSFGSGTSGWRGCD 179
DB 121 GFEPFLPGETYYTYSVPTPESSGQCRLQVSVCCCKERKSESNAHPVGSFGSGTSGWRGCD 179
Search completed: April 19, 2005, 23:22:25
Job time : 33.3289 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 22:12:51 ; Search time 14.1316 Seconds
(without alignments)
945.555 Million cell updates/sec

Title: US-09-904-954-4_COPY_1_179
Perfect score: 989
Sequence: 1 MRLPLRLRYLWMAAFLGSP.....SAHVPVGSRGSSTGSMRGGD 179

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	989	100.0	201	1	US-08-240-124-4 Sequence 4, Appli
2	989	100.0	201	1	US-08-453-943-4 Sequence 4, Appli
3	989	100.0	201	2	US-09-057-121-4 Sequence 4, Appli
4	989	100.0	201	3	US-03-358-734-4 Sequence 4, Appli
5	989	100.0	210	4	US-09-949-016-7162 Sequence 7162, Ap
6	971	98.2	201	4	US-09-214-631-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-240-124-4
; Sequence 4, Application US/08240124
; Patent No. 5516658
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
; TITLE OF INVENTION: RECEPTOR HERK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA

```

? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Apple System 7.1
? SOFTWARE: Microsoft Word for Apple, Version 5.1a
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/240,124
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/161,132
? FILING DATE: 03-DEC-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/114,426
? FILING DATE: 30-AUG-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/109,745
? FILING DATE: 20-AUG-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: SESE, KATHRYN A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2814-C
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELEEX: 756822
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 201 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
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? US-08-240-124-4
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? Query Match 100.0%; Score 989; DB 1; Length 201;
? Best Local Similarity 100.0%; Pred. No. 2.6e-107;
? Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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? Db QY 1 MRLPLRLRYLWMAAFLGSP...SARHVPVGSRGSSTGSMRGGD 60
? 1 MRLPLRLRYLWMAAFLGSP...SARHVPVGSRGSSTGSMRGGD 60
? Db QY 61 YBGPPEPGETALVWVMPGYE...SARHVPVGSRGSSTGSMRGGD 120
? 61 YBGPPEPGETALVWVMPGYE...SARHVPVGSRGSSTGSMRGGD 120
? Db QY 121 GFEPFLPEETYYISVPTPESSG...SARHVPVGSRGSSTGSMRGGD 179
? 121 GFEPFLPEETYYISVPTPESSG...SARHVPVGSRGSSTGSMRGGD 179
? Db QY 121 GFEPFLPEETYYISVPTPESSG...SARHVPVGSRGSSTGSMRGGD 179
? 121 GFEPFLPEETYYISVPTPESSG...SARHVPVGSRGSSTGSMRGGD 179
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? RESULT 2
? US-08-453-943-4
? Sequence 4, Application US/08453943
? Patent No. 5738844
? GENERAL INFORMATION:
? APPLICANT: BECKMANN, M. P.
? TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
? TITLE OF INVENTION: RECEPTOR HERK
? NUMBER OF SEQUENCES: 4
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: IMMUNEX CORPORATION
? STREET: 51 UNIVERSITY STREET
? CITY: SEATTLE
? STATE: WASHINGTON
? COUNTRY: USA
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Apple System 7.1

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SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
FILING DATE: 20-AUG-1993
APPLICATION NUMBER: US 08/109,745
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-943-4

Query Match Best Local Similarity 100.0%; Score 989; DB 1; Length 201;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MRLLPLRLTYMAAFLGSPPLRGGSSLRHYVWVWNSNPRLLRGDVAVELGINDYLDIYCPH 60
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Qy 61 YEGGPPPEPPEFTFALVMDWPGYSCQAEGRAYRKYRWCSPFGHVOPESEKIQRPFPFSL 120
Db 121 GFEFLPGETYYIISVTPPESSGQCLRLQVSVCCERKESASHPVGSPEGSGTSGWRGCD 179
Qy 121 GFEFLPGETYYIISVTPPESSGQCLRLQVSVCCERKESASHPVGSPEGSGTSGWRGCD 179

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
FILING DATE:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
FILING DATE: 20-AUG-1993
APPLICATION NUMBER: US 08/109,745
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-057-121-4

Query Match Best Local Similarity 100.0%; Score 989; DB 2; Length 201;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MRLLPLRLTYMAAFLGSPPLRGGSSLRHYVWVWNSNPRLLRGDVAVELGINDYLDIYCPH 60
Qy 1 MRLLPLRLTYMAAFLGSPPLRGGSSLRHYVWVWNSNPRLLRGDVAVELGINDYLDIYCPH 60
Db 61 YEGGPPPEPPEFTFALVMDWPGYSCQAEGRAYRKYRWCSPFGHVOPESEKIQRPFPFSL 120
Qy 61 YEGGPPPEPPEFTFALVMDWPGYSCQAEGRAYRKYRWCSPFGHVOPESEKIQRPFPFSL 120
Db 121 GFEFLPGETYYIISVTPPESSGQCLRLQVSVCCERKESASHPVGSPEGSGTSGWRGCD 179
Qy 121 GFEFLPGETYYIISVTPPESSGQCLRLQVSVCCERKESASHPVGSPEGSGTSGWRGCD 179

Query Match Best Local Similarity 100.0%; Score 989; DB 2; Length 201;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MRLLPLRLTYMAAFLGSPPLRGGSSLRHYVWVWNSNPRLLRGDVAVELGINDYLDIYCPH 60
Qy 1 MRLLPLRLTYMAAFLGSPPLRGGSSLRHYVWVWNSNPRLLRGDVAVELGINDYLDIYCPH 60
Db 61 YEGGPPPEPPEFTFALVMDWPGYSCQAEGRAYRKYRWCSPFGHVOPESEKIQRPFPFSL 120
Qy 61 YEGGPPPEPPEFTFALVMDWPGYSCQAEGRAYRKYRWCSPFGHVOPESEKIQRPFPFSL 120
Db 121 GFEFLPGETYYIISVTPPESSGQCLRLQVSVCCERKESASHPVGSPEGSGTSGWRGCD 179
Qy 121 GFEFLPGETYYIISVTPPESSGQCLRLQVSVCCERKESASHPVGSPEGSGTSGWRGCD 179

RESULT 3
US-09-057-121-4
Sequence 4, Application US/09057121
Patent No. 5969110
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,121

RESULT 4
US-09-358-734-4
Sequence 4, Application US/09358734
Patent No. 6274117
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
TITLE OF INVENTION: DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/358,734

APPLICATION NUMBER: 08/240,124
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/114,426
 FILING DATE: 30-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/109,745
 FILING DATE: 20-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: SEESE, KATHRYN A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2814-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 201 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-358-734-4

Query Match 100.0%; Score 989; DB 3; Length 201;
 Best Local Similarity 100.0%; Pred. No. 2,6e-107;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPLLRITVYVMAAFILGSPVLRGSSSLRHHVYVYVWNSNPRLLRGAAYVELGLNDYLDIVCPH 60
 DB 1 MRLPLLRITVYVMAAFILGSPVLRGSSSLRHHVYVYVWNSNPRLLRGAAYVELGLNDYLDIVCPH 60
 QY 61 YEGGPEPEGETFALVWVDPVYESSCAEGPRAYKRWVCSLPFGHVQFSEKIQRFPTPSSL 120
 DB 61 YEGGPEPEGETFALVWVDPVYESSCAEGPRAYKRWVCSLPFGHVQFSEKIQRFPTPSSL 120
 QY 121 GFERLPGERTYTYISVLPPESSGQCLRLQVSVCKEKRSBSAHFVGSFSGSSTGMRGSD 179
 DB 121 GFERLPGERTYTYISVLPPESSGQCLRLQVSVCKEKRSBSAHFVGSFSGSSTGMRGSD 179

RESULT 5
 US-09-949-016-7162
 ; Sequence 7162, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 7162
 ; LENGTH: 210
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-7162

Query Match 100.0%; Score 989; DB 4; Length 210;
 Best Local Similarity 100.0%; Pred. No. 2,8e-107;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPLLRITVYVMAAFILGSPVLRGSSSLRHHVYVYVWNSNPRLLRGAAYVELGLNDYLDIVCPH 60
 DB 10 MRLPLLRITVYVMAAFILGSPVLRGSSSLRHHVYVYVWNSNPRLLRGAAYVELGLNDYLDIVCPH 69

QY 61 YEGGPEPEGETFALVWVDPVYESSCAEGPRAYKRWVCSLPFGHVQFSEKIQRFPTPSSL 120
 DB 70 YEGGPEPEGETFALVWVDPVYESSCAEGPRAYKRWVCSLPFGHVQFSEKIQRFPTPSSL 129
 QY 121 GFERLPGERTYTYISVLPPESSGQCLRLQVSVCKEKRSBSAHFVGSFSGSSTGMRGSD 179
 DB 130 GFERLPGERTYTYISVLPPESSGQCLRLQVSVCKEKRSBSAHFVGSFSGSSTGMRGSD 188

RESULT 6
 US-09-214-631-8
 ; Sequence 8, Application US/09214631
 ; Patent No. 6413730
 ; GENERAL INFORMATION:
 ; APPLICANT: Holland, Sacha
 ; APPLICANT: Mamanu, Geradine
 ; APPLICANT: Pawson, Tony
 ; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
 ; BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
 ; TITLE OF INVENTION: TYROSINE KINASES
 ; FILE REFERENCE: 11757.23USWO
 ; CURRENT APPLICATION NUMBER: US/09/214,631
 ; CURRENT FILING DATE: 1999-03-12
 ; EARLIER APPLICATION NUMBER: PCT/CA97/00473
 ; EARLIER FILING DATE: 1997-07-04
 ; EARLIER APPLICATION NUMBER: 60/021,272
 ; EARLIER FILING DATE: 1996-07-05
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 201
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-214-631-8

Query Match 98.2%; Score 971; DB 4; Length 201;
 Best Local Similarity 98.3%; Pred. No. 3,3e-105;
 Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRLPLLRITVYVMAAFILGSPVLRGSSSLRHHVYVYVWNSNPRLLRGAAYVELGLNDYLDIVCPH 60
 DB 1 MRLPLLRITVYVMAAFILGSPVLRGSSSLRHHVYVYVWNSNPRLLRGAAYVELGLNDYLDIVCPH 60
 QY 61 YEGGPEPEGETFALVWVDPVYESSCAEGPRAYKRWVCSLPFGHVQFSEKIQRFPTPSSL 120
 DB 61 YEGGPEPEGETFALVWVDPVYESSCAEGPRAYKRWVCSLPFGHVQFSEKIQRFPTPSSL 120
 QY 121 GFERLPGERTYTYISVLPPESSGQCLRLQVSVCKEKRSBSAHFVGSFSGSSTGMRGSD 179
 DB 121 GFERLPGERTYTYISVLPPESSGQCLRLQVSVCKEKRSBSAHFVGSFSGSSTGMRGSD 179

Search completed: April 19, 2005, 23:19:49
 Job time: 14.1316 secs

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OM protein - protein search, using sw model

Run on: April 19, 2005, 15:35:11 ; Search time 48.9895 Seconds
(without alignments)
1413.163 Million cell updates/sec

Title: US-09-904-954-4_COPY_1_179

Perfect score: 989
Sequence: 1 MRLPLRLRTVLMWAAPLGGSP.....SAHPVGSPPSSGTSQWRGSD 179

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 89%
Maximum Match 100%
Listing first 1500 summaries

- Database :
- 1: A_Geneseq_16Dec04:*
 - 2: geneseqp1980s:*
 - 3: geneseqp1990s:*
 - 4: geneseqp2000s:*
 - 5: geneseqp2001s:*
 - 6: geneseqp2002s:*
 - 7: geneseqp2003as:*
 - 8: geneseqp2003bs:*
 - 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	989	100.0	201	2 AAR71482	Human hek

ALIGNMENTS

RESULT 1
AAR71482
ID AAR71482 standard; protein; 201 AA.
AC AAR71482;
XX
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-1995 (first entry)
XX
XX
DE Human hek-L protein.
XX
XX
KM Ligand; cell surface; tyrosine kinase receptor; tumorigenesis; immunogen.
OS Homo sapiens.
XX
XX
PH Key
PH Peptide
FT Location/Qualifiers
FT /note= "signal peptide"
FT Protein
FT 23..201

XX XX
FN MO9506065-A1.
XX PD
PD 02-MAR-1995.
XX PF
PF 17-AUG-1994; 94WO-US009282.
XX PR
PR 20-AUG-1993; 93US-00109745.
PR 30-AUG-1993; 93US-00114426.
PR 03-DEC-1993; 93US-00161132.
PR 09-MAY-1994; 94US-00240124.
PA (IMMV) IMMUNEX CORP.
PI Beckmann MP, Carretti DP;
XX WP1; 1995-106811/14.
DR N-PSDB; AAQ85888.
XX
XX
PT New isolated DNA encoding hek-L protein or its fusion products - useful
PT as assay reagent or for carrying therapeutic and diagnostic compounds to
PT leukaemia cells.
XX
XX
PS Claim 21; Page 38; 45pp; English.
XX
XX
CC The sequence is that of a novel protein designated hek-L, a protein that
CC can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the
CC first known ligand for hek and can be used to study cellular processes
CC regulated by hek (which may be involved in tumorigenesis). It is also an
CC immunogen for antibody production, as a reagent for detecting hek or hek-
CC L in in vitro assays, to determine binding of hek proteins, to purify hek
CC proteins, and to carry diagnostic or cytotoxic agents to particular
CC leukaemia cells that express the hek antigen. Hek-L also binds the e1k
CC tyrosine kinase receptors. See also AAR71481. (Updated on 25-MAR-2003 to
CC correct FN field.)
XX
XX
SQ Sequence 201 AA;
Query Match 100.0%; Score 989; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.4e-102; Indels 0; Gaps 0;
Matches 179; Conservative 0; Mismatches 0;

Qy 1 MRLPLRLRTVLMWAAPLGGSP...
Db 1 MRLPLRLRTVLMWAAPLGGSP...
Qy 61 YEGGPPGPEGPEPALVWVDPGYESSQABGPRAYKRWVCSLPGHVQFSEKIQRFPPSL 120
Db 61 YEGGPPGPEGPEPALVWVDPGYESSQABGPRAYKRWVCSLPGHVQFSEKIQRFPPSL 120
Qy 121 GFERLPGETYYTYSVPTPSSGQCLRLQVSVCKEKRESANHPVGSGBEGTSGWRGSD 179
Db 121 GFERLPGETYYTYSVPTPSSGQCLRLQVSVCKEKRESANHPVGSGBEGTSGWRGSD 179

Search completed: April 19, 2005, 23:13:33
Job time : 48.9895 secs

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OY 241 TTGGCCATGTTCAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT
 DB 334 TTGGCCATGTTCAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT
 OY 301 GAGTCTTAACTTCTGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT
 DB 394 GAGTCTTAACTTCTGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT
 OY 361 CAGTGTTCAGGCTTCAAGAGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT
 DB 454 CAGTGTTCAGGCTTCAAGAGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT
 OY 421 CCTGTGGGAGAGCCCTTGGAGAGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT
 DB 514 CCTGTGGGAGAGCCCTTGGAGAGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT

RESULT 2
 AB234863 ID AB234863 standard; cDNA, 1181 BP.
 AC AB234863;
 AT 04-FEB-2003 (first entry)
 DE Coding sequence SEQ ID 221, differentially expressed in osteogenesis.

KW Osteopaplastic; osteogenesis modulator; gene therapy; osteogenesis;
 KM osteoporosis; bone disease; upregulator; human; ephrin-ephrin; ss.
 XX Homo sapiens.
 OS M0200281745-A2.
 PN 17-OCT-2002.
 PD 05-APR-2002; 2002MO-1B002211.
 PR 05-APR-2001; 2001US-0281400P.
 PI (AVET) AVENTIS PHARMA SA.
 PI Garcia T, Roman Roman S, Baron R, Cali K, Theilhaber J;
 PI Connolly T, Jackson A, Bushnell SE, Rawadi G;
 DR WPI; 2003-058567/05.

Novel isolated nucleic acid upregulated/downregulated in osteogenesis, useful for bone disease therapy in subject.
 Claim 1; Page 214; 237pp; English.
 The present invention relates to novel nucleotide sequences, which are differentially expressed in models of osteogenesis upon being put in contact with a stimulator of osteogenesis. The present sequence is one of such sequences. This sequence can be used for diagnosing osteoporosis/bone disease in a patient, promoting osteogenesis and/or preventing osteoporosis/bone disease. The present sequence encodes a Ephrin-ephrin family protein.

Sequence 1181 BP; 234 A; 353 C; 331 G; 263 T; 0 U; 0 Other;
 Query Match Best Local Similarity 100.0%; Score 480; DB 8; Length 1181;
 Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 94 GGCTCCAGCCCTCCGACCGTAGTCTACTGGAAGTCCAGTAAACCCAGGTTGGTTCAGAGA 60
 DB 61 GAGCGCGTGTGAGAGCTGGGCTCAAGATTAAGATTTGCTGCCCCCACTACAGAA 120
 OY 154 GAGCGCGTGTGAGAGCTGGGCTCAAGATTAAGATTTGCTGCCCCCACTACAGAA 213

OY 121 GGCCCAAGGAGCCCTGAGAGAGAGAGACTTGGTCTGTTGTAATGTTGAGATTCAGGCGCAAGC 180
 DB 214 GGCCCAAGGAGCCCTGAGAGAGAGAGACTTGGTCTGTTGTAATGTTGAGATTCAGGCGCAAGC 180
 OY 181 TATGAGTCTCCAGGAG 273
 DB 274 TATGAGTCTCCAGGAG 273
 OY 241 TTGGCCATGTTCAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT 300
 DB 334 TTGGCCATGTTCAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT 300
 OY 301 GAGTCTTAACTTCTGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT 393
 DB 394 GAGTCTTAACTTCTGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT 393
 OY 361 CAGTGTTCAGGCTTCAAGAGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT 420
 DB 454 CAGTGTTCAGGCTTCAAGAGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT 420
 OY 421 CCTGTGGGAGAGCCCTTGGAGAGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT 513
 DB 514 CCTGTGGGAGAGCCCTTGGAGAGAGAGACTTAATTAATTCCTGAGAGAGATTTCAGCGCTTCAACCTTTCTCCCTGGGCTTT 513

RESULT 3
 ABV78135 ID ABV78135 standard; DNA, 606 BP.
 AC ABV78135;
 AT 15-NOV-2002 (first entry)
 DE Human ephrin-A3 DNA SEQ ID NO 19.
 DE RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
 KW RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
 KM virucide; protozoacide; gene; ds.
 OS Homo sapiens.
 OS M0200255693-A2.
 PN 18-JUL-2002.
 PD 09-JAN-2002; 2002MO-EP000152.
 PR 09-JAN-2001; 2001DE-01000586.
 PR 26-OCT-2001; 2001DE-01055280.
 PR 29-NOV-2001; 2001DE-01058411.
 PR 07-DEC-2001; 2001DE-01060151.
 PI (RIBO-) RIBOPHARMA AG.
 PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
 DR WPI; 2002-590671/63.

Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to the target and having an overhang.
 Claim 10; Page 123; 203pp; German.
 The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (asi) of dsRNA is complementary to (I) and at least one end of dsRNA has an overhang of 1-4 nucleotides. The method is used to inhibit dsRNA expression of a wide range of genes, e.g. oncogenes, cytokine genes, pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression.

The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (asi) of dsRNA is complementary to (I) and at least one end of dsRNA has an overhang of 1-4 nucleotides. The method is used to inhibit dsRNA expression of a wide range of genes, e.g. oncogenes, cytokine genes, pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression.

CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX

Query Match 99.7%; Score 478.4; DB 6; Length 606;
Best Local Similarity 99.8%; Pred. No. 6,4e-129;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GGGTCCAGCCTCCGCCACGTAAGTCTGTAAGTCCGCAAGCCAGGTTCTTCGAGGA 60
67 GGGTCCAGCCTCCGCCACGTAAGTCTGTAAGTCCGCAAGCCAGGTTCTTCGAGGA 126
61 GAGCCGCTGGTGAAGTGGGGCTCAACGATTTACTAAGCAATGTCGTCGCTCCCACTAGAA 120
127 GAGCCGCTGGTGAAGTGGGGCTCAACGATTTACTAAGCAATGTCGTCGCTCCCACTAGAA 186
121 GGGCCAGAGGCCCCCTGAGAGGCCCCCGAGACGTTTGTCTTTGTAACATGTGGACTGGCCAGGC 180
187 GGGCCAGAGGCCCCCTGAGAGGCCCCCGAGACGTTTGTCTTTGTAACATGTGGACTGGCCAGGC 246
181 TATGAGTCTCTGCCAGGAGAGGGCCCCGGGCTTACAAGCGCTGGTGTGCTCCCTGCCC 240
247 TATGAGTCTCTGCCAGGAGAGGGCCCCGGGCTTACAAGCGCTGGTGTGCTCCCTGCCC 306
241 TTTGGCCATGTTCAATTTCTAGAGAAATTCAGCGCTTTCACACCTTTCTCCCGGGTTT 300
307 TTTGGCCATGTTCAATTTCTAGAGAAATTCAGCGCTTTCACACCTTTCTCCCGGGTTT 366
301 GAGTTCCTTACCTGAGAGACTTACTACTAATCATCTCGGTGCCCACTCCAGAGAGTTCTGGC 360
367 GAGTTCCTTACCTGAGAGACTTACTACTAATCATCTCGGTGCCCACTCCAGAGAGTTCTGGC 426
361 GAGTTCCTTACCTGAGAGACTTACTACTAATCATCTCGGTGCCCACTCCAGAGAGTTCTGGC 420
427 CAGTGTCTTGAAGGCTCCAGGAGTGTCTGTCTGTCTGCAAGGAGAAAGTCTGAGTCAAGCCAT 486
421 CCGTGTGGAGAGCCCTGAGAGAGTGGCAATCAAGGGTGGGAGGGGGGAGCACTCCAGC 480
487 CCTGTGGAGAGCCCTGAGAGAGTGGCAATCAAGGGTGGGAGGGGGGAGCACTCCAGC 546

RESULT 4
ABZ35711 standard; DNA; 606 BP.
ABZ35711,
ABZ35711,
07-FEB-2003 (first entry)
Human ephrin A3 encoding polynucleotide SEQ ID NO 19.

XX Inhibiting expression of target genes, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.
PS Claim 13; Page 19-20; 100pp; German.

The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligonucleotides (dsRNA1 and 11), both
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNA1 and 11 are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumors
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention

Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other;
Query Match 99.7%; Score 478.4; DB 6; Length 606;
Best Local Similarity 99.8%; Pred. No. 6,4e-129;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 GGGTCCAGCCTCCGCCACGTAAGTCTGTAAGTCCGCAAGCCAGGTTCTTCGAGGA 60
67 GGGTCCAGCCTCCGCCACGTAAGTCTGTAAGTCCGCAAGCCAGGTTCTTCGAGGA 126
61 GAGCCGCTGGTGAAGTGGGGCTCAACGATTTACTAAGCAATGTCGTCGCTCCCACTAGAA 120
127 GAGCCGCTGGTGAAGTGGGGCTCAACGATTTACTAAGCAATGTCGTCGCTCCCACTAGAA 186
121 GGGCCAGAGGCCCCCTGAGAGGCCCCCGAGACGTTTGTCTTTGTAACATGTGGACTGGCCAGGC 180
187 GGGCCAGAGGCCCCCTGAGAGGCCCCCGAGACGTTTGTCTTTGTAACATGTGGACTGGCCAGGC 246
181 TATGAGTCTCTGCCAGGAGAGGGCCCCGGGCTTACAAGCGCTGGTGTGCTCCCTGCCC 240
247 TATGAGTCTCTGCCAGGAGAGGGCCCCGGGCTTACAAGCGCTGGTGTGCTCCCTGCCC 306
241 TTTGGCCATGTTCAATTTCTAGAGAAATTCAGCGCTTTCACACCTTTCTCCCGGGTTT 300
307 TTTGGCCATGTTCAATTTCTAGAGAAATTCAGCGCTTTCACACCTTTCTCCCGGGTTT 366
301 GAGTTCCTTACCTGAGAGACTTACTACTAATCATCTCGGTGCCCACTCCAGAGAGTTCTGGC 360
367 GAGTTCCTTACCTGAGAGACTTACTACTAATCATCTCGGTGCCCACTCCAGAGAGTTCTGGC 426
361 GAGTTCCTTACCTGAGAGACTTACTACTAATCATCTCGGTGCCCACTCCAGAGAGTTCTGGC 420
427 CAGTGTCTTGAAGGCTCCAGGAGTGTCTGTCTGTCTGCAAGGAGAAAGTCTGAGTCAAGCCAT 486
421 CCGTGTGGAGAGCCCTGAGAGAGTGGCAATCAAGGGTGGGAGGGGGGAGCACTCCAGC 480
487 CCTGTGGAGAGCCCTGAGAGAGTGGCAATCAAGGGTGGGAGGGGGGAGCACTCCAGC 546

RESULT 5
ABX09954 standard; DNA; 606 BP.
ABX09954,
ABX09954,
23-JAN-2003 (first entry)
Human ephrin A3 DNA fragment SEQ ID 19.
Oligonucleotide; interferon; oncogene; cytokine; Id; developmental;
PI Human ephrin A3 encoding polynucleotide SEQ ID NO 19.

XX OS Homo sapiens.
 XX PN DE10100587-C1.
 XX PD 21-NOV-2002.
 XX PF 09-JAN-2001; 2001DE-01000587.
 XX PR 09-JAN-2001; 2001DE-01000587.
 XX PA (RIBO-) RIBOPHARMA AG.
 XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
 XX DR MPI, 2002-742209/81.
 XX PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by
 XX PR introduction of complementary double-stranded oligoribonucleotide, after
 XX PS treating the cell with interferon.
 XX PS Disclosure; Page 24-25; 98pp; German.
 CC This invention describes a novel method for inhibiting expression of a
 CC target gene by introducing into the cell that contains the target gene at
 CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
 CC structure of not more than 49 consecutive nucleotides (nt), where at
 CC least a segment of one strand of the ds structure is complementary with
 CC the target gene and the cells are treated with interferon before
 CC introduction of dsRNA. The method is used to inhibit expression of
 CC target genes, particularly oncogenes, cytokine genes, Id (not defined)
 CC protein genes, developmental or prion genes, or genes expressed in
 CC pathogenic organisms (particularly plasmidial) or in viruses or viroids
 CC (pathogenic in humans, animals or plants). Treating the cells with
 CC interferon greatly increases the extent to which dsRNA can inhibit
 CC expression of the target genes, and the effect is even greater when dsRNA
 CC are modified to increase their stability. ABX09336-ABX10075 represent
 CC gene fragments used to illustrate the method of the invention
 CC XX
 CC XX Sequence 606 BP; 96 A; 191 C; 175 G; 144 T; 0 U; 0 Other;
 CC XX

Query Match Best Local Similarity 99.7%; Score 478.4; DB 6; Length 606;
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTCCAGCCCTCGCCAGCACTGATCTTCTGAACTCCAGTAAACCCAGGTTGCTTCAGGA 60
 Db |GGCTCCAGCCCTCGCCAGCACTGATCTTCTGAACTCCAGTAAACCCAGGTTGCTTCAGGA 60
 QY 67 GGCTCCAGCCCTCGCCAGCACTGATCTTCTGAACTCCAGTAAACCCAGGTTGCTTCAGGA 126
 Db |GGCTCCAGCCCTCGCCAGCACTGATCTTCTGAACTCCAGTAAACCCAGGTTGCTTCAGGA 126
 QY 61 GAGCCGCTGATGAGCTGGGCTCAACGATTTACTAGACATTTGTCGCCCACTACGAA 120
 Db |GAGCCGCTGATGAGCTGGGCTCAACGATTTACTAGACATTTGTCGCCCACTACGAA 120
 QY 127 GAGCCGCTGATGAGCTGGGCTCAACGATTTACTAGACATTTGTCGCCCACTACGAA 186
 Db |GAGCCGCTGATGAGCTGGGCTCAACGATTTACTAGACATTTGTCGCCCACTACGAA 186
 QY 121 GGCCCAAGGGCCCTCGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 180
 Db |GGCCCAAGGGCCCTCGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 180
 QY 187 GGCCCAAGGGCCCTCGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 246
 Db |GGCCCAAGGGCCCTCGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 246
 QY 181 TATGAGTCTCTGCAAGCAAGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 240
 Db |TATGAGTCTCTGCAAGCAAGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 240
 QY 247 TATGAGTCTCTGCAAGCAAGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 306
 Db |TATGAGTCTCTGCAAGCAAGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 306
 QY 241 TTTGGCCATGTTCAATTTCTCAAGAAAGATTCAAGCGCTTTCACACCCCTTCCCTCGGCTTT 300
 Db |TTTGGCCATGTTCAATTTCTCAAGAAAGATTCAAGCGCTTTCACACCCCTTCCCTCGGCTTT 300
 QY 307 TTTGGCCATGTTCAATTTCTCAAGAAAGATTCAAGCGCTTTCACACCCCTTCCCTCGGCTTT 366
 Db |TTTGGCCATGTTCAATTTCTCAAGAAAGATTCAAGCGCTTTCACACCCCTTCCCTCGGCTTT 366
 QY 301 GAGTTTCTTACCTGGAGACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 360
 Db |GAGTTTCTTACCTGGAGACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 360
 QY 367 GAGTTTCTTACCTGGAGACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 426
 Db |GAGTTTCTTACCTGGAGACTTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 426
 QY 361 CAGTGTGAGAGGCTCCAGGATGCTGTCCTGCAAGAGAGAAAGTCTGAGTCCAGCCAT 420
 Db |CAGTGTGAGAGGCTCCAGGATGCTGTCCTGCAAGAGAGAAAGTCTGAGTCCAGCCAT 420
 QY 427 CAGTGTGAGAGGCTCCAGGATGCTGTCCTGCAAGAGAGAAAGTCTGAGTCCAGCCAT 486
 Db |CAGTGTGAGAGGCTCCAGGATGCTGTCCTGCAAGAGAGAAAGTCTGAGTCCAGCCAT 486

QY 421 CCTGTGGAGAGCCCTCGAGAGAGATGTCGCACATCAGGGTGGCCAGAGGGGCACTCCAGC 480
 Db |CCTGTGGAGAGCCCTCGAGAGAGATGTCGCACATCAGGGTGGCCAGAGGGGCACTCCAGC 480
 RESULT 6
 ABL91676
 ID ABL91676 standard; DNA; 606 BP.
 XX
 XX ABL91676;
 AC
 AC 28-MAY-2002 (first entry)
 DT
 XX Human polynucleotide SEQ ID NO 19.
 DE
 XX
 XX Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
 KM Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
 KW cytosol; viricide; protozoacide; antibacterial; ds.
 XX
 OS Homo sapiens.
 OS
 XX
 XX DE10100586-C1.
 PN
 BD 11-APR-2002.
 XX
 XX 09-JAN-2001; 2001DE-01000586.
 PP
 XX 09-JAN-2001; 2001DE-01000586.
 PR
 XX (RIBO-) RIBOPHARMA AG.
 PA
 XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
 PI
 XX MPI, 2002-270454/32.
 DR
 XX
 XX Inhibiting gene expression in cells, useful for e.g. treating tumors, by
 XX PT introducing double-stranded complementary oligoRNA having unpaired
 XX PR terminal bases.
 XX PS
 XX Claim 13; Page 20-21; 104pp; German.
 XX
 CC The invention relates to a method for inhibiting expression of a target
 CC gene (ABL91676-ABL91797) in a cell by introducing at least one
 CC oligoribonucleotide that has a double-stranded structure consisting of at
 CC most 49 sequential nucleotide pairs, with at least part of one strand
 CC complementary with the target gene and has at least one end a single-
 CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
 CC antisense inhibition of gene expression useful e.g. for treating tumors
 CC but the oligoribonucleotide of gene expression may also be directed against
 CC in pathogens (e.g. Plasmodium or viruses/viroids), pathogenic on humans,
 CC animals or plants) or against cytokine, Id, developmental or prion genes.
 CC The method provides more effective inhibition of gene expression than use
 CC of known oligonucleotides, probably because the unpaired overhang
 CC increases stability and thus intracellular concentration
 CC XX

Query Match Best Local Similarity 99.7%; Score 478.4; DB 6; Length 606;
 Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTCCAGCCCTCGCCAGCACTGATCTTCTGAACTCCAGTAAACCCAGGTTGCTTCAGGA 60
 Db |GGCTCCAGCCCTCGCCAGCACTGATCTTCTGAACTCCAGTAAACCCAGGTTGCTTCAGGA 60
 QY 67 GGCTCCAGCCCTCGCCAGCACTGATCTTCTGAACTCCAGTAAACCCAGGTTGCTTCAGGA 126
 Db |GGCTCCAGCCCTCGCCAGCACTGATCTTCTGAACTCCAGTAAACCCAGGTTGCTTCAGGA 126
 QY 61 GAGCCGCTGATGAGCTGGGCTCAACGATTTACTAGACATTTGTCGCCCACTACGAA 120
 Db |GAGCCGCTGATGAGCTGGGCTCAACGATTTACTAGACATTTGTCGCCCACTACGAA 120
 QY 127 GAGCCGCTGATGAGCTGGGCTCAACGATTTACTAGACATTTGTCGCCCACTACGAA 186
 Db |GAGCCGCTGATGAGCTGGGCTCAACGATTTACTAGACATTTGTCGCCCACTACGAA 186
 QY 121 GGCCCAAGGGCCCTCGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 180
 Db |GGCCCAAGGGCCCTCGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 180
 QY 187 GGCCCAAGGGCCCTCGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 246
 Db |GGCCCAAGGGCCCTCGAGGGCCCGGAGACGTTTGTGTAACATGTTGAGTCCAGCCAGGC 246

QY 181 TANGAGTCTGCGCAGGAGGCCCCCGGCTTACAAGCGTGGTGTGCTCCCTGCC 240
 DB 247 TATGAGTCTGCGCAGGAGGCCCCCGGCTTACAAGCGTGGTGTGCTCCCTGCC 306
 QY 241 TTTGGCCATGTTCAATTCTCAGAGAGATTCAAGGCTTCAACCTTTCTCCCTGGCTTT 300
 DB 307 TTTGGCCATGTTCAATTCTCAGAGAGATTCAAGGCTTCAACCTTTCTCCCTGGCTTT 366
 QY 301 GAGTCTTACTGGAGAGACTTACTACTACTACTCTCCGCTCCACTCCAGAGAGTTCTGGC 360
 DB 367 GAGTCTTACTGGAGAGACTTACTACTACTACTCTCCGCTCCACTCCAGAGAGTTCTGGC 426
 QY 361 CAGTCTTGAAGGCTCCAGGCTGTCTGTCTGCTGAAGAGAGAGAGTCTGAGTCAAGCCAT 420
 DB 427 CAGTCTTGAAGGCTCCAGGCTGTCTGTCTGCTGAAGAGAGAGTCTGAGTCAAGCCAT 486
 QY 421 CCGTGTGGAGCCCTGGAGAGAGTGGACATCAGGGTGGCCGAGGGGGGACACTCCGAGC 480
 DB 487 CCGTGTGGAGCCCTGGAGAGAGTGGACATCAGGGTGGCCGAGGGGGGACACTCCGAGC 546

RESULT 7
 ADN02769 ID ADN02769 standard; cDNA; 770 BP.
 XX AC ADN02769;
 DT 01-JUL-2004 (first entry)
 XX DE Human receptor and membrane-associated protein cDNA #22.
 XX OS Homo sapiens.

XX db; gene: cytostatic; antiarteriosclerotic; anti-HIV, cerebroprotective;
 KW antiParkinsonian; nootropic; neuroprotective; immunosuppressive;
 KW antiinflammatory; antiallergic; anabolic; hypertensive; anorectic;
 KW antidiabetic; gene therapy; receptor and membrane-associated protein;
 KW REMAP; diagnosing; cancer; atherosclerosis; AIDS; allergy;
 KW Parkinson's disease; Alzheimer's disease; stroke; Addison's disease;
 KW obesity; diabetes; microarray; gene expression; receptor.
 XX OS Homo sapiens.
 XX PN MO2004029218-A2.
 XX PD 08-APR-2004.
 XX PF 26-SEP-2003; 2003WO-US030894.
 XX PR 27-SEP-2002; 2002US-0414302P.
 PR 11-OCT-2002; 2002US-0417797P.
 PR 16-OCT-2002; 2002US-0419217P.
 PR 29-OCT-2002; 2002US-0422375P.
 PR 07-NOV-2002; 2002US-0424799P.
 XX PA (INCY-) INCYTE CORP.
 XX PI Marguis JP, Tean UK, Lee SY, Richardson TW, Chawla NK,
 PI Hafalila AJA, Becha SD, Ramkumar J, Khare R, Tang YT, Yue H,
 PI Baughn MR, Elliott VS, Swarnakar A, Lu DAM, Pollock JL,
 PI Thangavelu K, Gietzen KJ, Blake JF, Ison CH;
 DR WPI: 2004-316100/29.
 DR P-PSDB; ADN027719.
 XX PT New human receptors and membrane-associated proteins and polynucleotides
 PT for diagnosing, preventing or treating diseases associated with aberrant
 PT protein expression, e.g. cancer, atherosclerosis, AIDS, stroke or
 PT diabetes.
 XX PS Claim 5; SEQ ID NO 72; 268bp; English.
 XX CC The invention relates to novel human receptor and membrane-associated
 CC protein (REMAP) and the genes encoding them, a naturally-occurring amino
 CC acid sequence that is at least 90% to at least 98% identical any of the

CC amino acid sequences cited above; or a biologically active or immunogenic
 CC fragment of the polypeptide. The specification also discloses a naturally
 CC occurring polynucleotide sequence that is at least 90% to at least 98%
 CC identical to any of the nucleotide sequences cited above; their
 CC complements or an RNA equivalent. The composition and methods are useful
 CC for diagnosing, preventing or treating diseases or conditions associated
 CC with aberrant expression of REMAP, such as cell proliferative (e.g.
 CC cancer or atherosclerosis), autoimmune/inflammatory (e.g. AIDS or
 CC allergies), neurological (e.g. Parkinson's disease, Alzheimer's disease
 CC or stroke), metabolic (e.g. Addison's disease or obesity), developmental
 CC or endocrine (e.g. diabetes) disorders. These may also be used for
 CC assessing the effects of exogenous compounds on the expression of nucleic
 CC acid and amino acid sequences of REMAP. The REMAP or its fragments are
 CC also useful in screening compounds for effectiveness as agonist or
 CC antagonist of the polypeptides, or in altering the expression of the
 CC target polynucleotide and compounds that specifically bind to or modulate
 CC the activity of the polypeptide. The microarray is useful in monitoring
 CC or measuring protein-protein interactions, drug-target interactions, and
 CC gene expression profiles. This sequence corresponds to the cDNA encoding
 CC one of the proteins of the invention.

XX SQ Sequence 770 BP; 134 A; 242 C; 213 G; 181 T; 0 U; 0 Other;
 Query Match 90.2%; Score 432.8; DB 12; Length 770;
 Best Local Similarity 98.4%; Pred. No. 1.3e-115;
 Matches 437; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 37 AGTAAACCCAGGTTGCTTGGAGAGAGCCGCTGGTGGAGTGGGCTCAAGATTAACCTTA 96
 DB 252 AGTCTGGCAGGAGTGGCTTTCAGAGAGAGCCGCTGGTGGAGTGGGCTCAAGATTAACCTTA 311
 QY 97 GACATTTGTCGCCCCCACTACGAAAGGCCAGGGCCCCCTTGAAGGCCCGGAGAGCTTTGCT 156
 DB 312 GACATTTGTCGCCCCCACTACGAAAGGCCAGGGCCCCCTTGAAGGCCCGGAGAGCTTTGCT 371
 QY 157 TTGTAACATGTTGAGCTGGCCAGGCTATGAGTCTCTGCAAGGAGAGGCCCCGGGCTTAC 216
 DB 372 TTGTAACATGTTGAGCTGGCCAGGCTATGAGTCTCTGCAAGGAGAGGCCCCGGGCTTAC 431
 QY 217 AAGCGCTGGTGTGCTCCCTGCGCTTTGGCCATGTTCAATTTCTCAGAGAAAGATTGAGCGC 276
 DB 432 AAGCGCTGGTGTGCTCCCTGCGCTTTGGCCATGTTCAATTTCTCAGAGAAAGATTGAGCGC 491
 QY 277 TTCAACCTTTTCCCTCGGCTTTGAGTTCTTACCTTGAAGAGACTTACTACTACTCTCG 336
 DB 492 TTCAACCTTTTCCCTCGGCTTTGAGTTCTTACCTTGAAGAGACTTACTACTACTCTCG 551
 QY 337 GTGCCCACTCCAGAGAGTCTGGCCAGTGTCTTGAAGGCTCCAGGCTGTCTGTGCTGCAAG 396
 DB 552 GTGCCCACTCCAGAGAGTCTGGCCAGTGTCTTGAAGGCTCCAGGCTGTCTGTGCTGCAAG 611
 QY 397 GAGAGGAAAGTCTGAGTCAAGCCATCTGTTGGAGCCCTGAGAGAGTGGCACTCAGGG 456
 DB 612 GAGAGGAAAGTCTGAGTCAAGCCATCTGTTGGAGCCCTGAGAGAGTGGCACTCAGGG 671
 QY 457 TGGCGAGGGGGGAGCACTCCGAGC 480
 DB 672 TGGCGAGGGGGGAGCACTCCGAGC 695

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